************************** *************** (MT)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Nov 2 16:31:05 1998; MasPar time 19.22 Seconds 691.579 Million cell updates/sec

Tabular output not generated.

Title:

Description: erfect Score: equence: >US-08-906-365-2 (1-530) from US08906365.pep 3904 1 MDIKNSPSSLNSPSSYNCSQ......ECSPAEDSKSKEGSQNPQSQ 530

Scoring table: PAM 150 Gap 11

Searched: 69111 seqs, 25083644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot35 1:swiss1

Statistics: Mean 50.804; Variance 83.063; scale 0.612

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2221185544321 22212865443221	Result No.
1698 1693 1663 1663 1591 1591 1591 1591 1591 680 680 681 666 668 668 668 67 697 697	Score
43.5 42.6 42.4 42.4 41.4 41.4 41.4 41.7 117.7 117.7 117.7 115.6 115.7 115.7 115.7 115.7	Query Match
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ALIGNMENTS

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P03372;
VARIANT ALA-447.
MEDLINE; 9225065
REESE J.C., KAT2
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SCHWABE J.W.E., NEUHAUS D.,
NATURE 348:458-461(1990).
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MEDLINE; 86122927.
GREERE G.L., GILMA P., WATERFIELD
SCIENCE 231:1150-1154(1986).
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MEDLINE; 90005402.
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LAST SEQUENCE UPDATE)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSFAC;
   428
                       477
                                           369
                                                                417
                                                                                     309
                                                                                                           357
                                                                                                                                255
                                                                                                                                                      298
                                                                                                                                                                           202
                                                                                                                                                                                                238
                                                                                                                                                                                                                      142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.

- IN THE ABSENCE OF LIGAND, STEROID HORMONE RECEPTORS ARE THOUGHT TO BE WEAKLY ASSOCIATED WITH NUCLEAR COMPONENTS; HORMONE BINDING GREATLY INCREASES RECEPTOR AFFINITY. THE HORMONE-RECEPTOR COMPLEX APPEARS TO RECOGNIZE DISCRETE DNA SEQUENCES UPSTREAM OF TRANSCRIPTIONAL START SITES.

SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETTANCYON NUCLEAR HORMONE RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: NUCLEAR.
DOMAIN: COMPOSED OF THREE DOMAINS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                      SKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSC
                                                                                                                                                                                                                                SAKETRYCAVCNDYASGYHYGVWSCEGCKAFFKRSIQGHNDYMCPATNQCTIDKNRRKSC
  ### HLINAVIDALVWYIAKSGISSQQQSMRLANLLMLLSHVRHASNKGMEHLLNWKCKNVVPV
                     RVLDKITDTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPL
                                                      CVEGMVEIFDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIH
                                                                                     MISWAKKIPGFVELSLFDQVRLLESCWMEVLMMGLMWRSIDHPGKLIFAPDLVLDRDEGK
                                                                                                MINWAKRVPGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGK 416
                                                                                                                                V-RELL--LD-ALSPEQLVLTLLEAEPPHVLISR--PSAPFTEASMMMSLTKLADKELVH
                                                                                                                                           IKRSKKNSLALSLTADQMVSALLDAEPP-ILYSEYDPTRPFSEASMMGLLTNLADRELVH
                                                                                                                                                                                               QACRLRKCYEVGMMKGGIRKDRRGGRMLKHKRQRDDGEGRGEVGSAGDMRAANLWPSPLM
                                          CVEGILEIFDMLLATTSRFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDA-DSSRKLA
                                                                                                                                                                          QACRIRKCYEVGMVKCGSRRERCGYRIVR -- RQRSADE-QIHCAGKA-KRSGG--HAP-R
                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00031; NUCLEAR_RECEPTOR; 1.
TRANSCRIPTION REGULATION; DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T00261; -
                                                                                                                                                                                                                                                                                                         595
                                                                                                                                                                                                                                                                                                                                                                                   185
185
221
251
311
160
400
                                                                                                                                                                                                                                                                                                                                        447
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STEROID-BINDING; POLYMORPHISM.

1 184 MODULATING.
                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                         A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267:9868-9873(1992).
                                                                                                                                                                                                                                                                         43.4%;
                                                                                                                                                                                                                                                                                                                                                                                   184
250
205
245
310
310
160
400
                                                                                                                                                                                                                                                                                                                                        447
                                                                                                                                                                                                                                                                                                         66216
                                                                                                                                                                                                                                                                                                         ₩;
                                                                                                                                                                                                                                                                                                                                                                               HINGE.
STEROID-BINDING.
G -> C.
G -> V (DESTABILIZES T
                                                                                                                                                                                                                                                                         Score 1693;
Pred. No. 0.
                                                                                                                                                                                                                                                              98;
                                                                                                                                                                                                                                                                                                                                                  DECREASES
25 DEGREES
CELSIUS).
                                                                                                                                                                                                                                                                                                                   BINDING
                                                                                                                                                                                                                                                                                                                            C -> A (LOSS OF HORMONE BINDING AND TEMPERATURE-SENSITIVE LOSS:
                                                                                                                                                                                                                                                                                                                                                                                                                           C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                    C4-TYPE ZINC C4-TYPE.
                                                                                                                                                                                                                                                                                                         D6945BB9
                                                                                                                                                                                                                                                                                                                                                            DEGREES
                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                      ESTABILIZES THE RECEPTOR AND ITS AFFINITY FOR ESTRADIOL
                                                                                                                                                                                                                                                                          DB 1;
.00e+00;
                                                                                                                                                                                                                                                                                                         CRC32;
                                                                                                                                                                                                                                                                                                                                                             CELSIUS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FINGERS
                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                             BUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEAR
                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TWO).
                                                                                                                                                                                                                                                                                                                                                             TON
                                                                                                                                                                                                                                                                                                                                                             ΑT
                                                                                                                                                                                                                                                              17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN;
                                                                                                                                                                                                                                                                                                                              G CAPACITY
                                                                                                                                                                                                                                                                                                                                                             4
                                                                                                                                                                                                                                                                                                                                                             DEGREES
                                                                                                                                                                                                                                                              Gaps
                                                                 476
                                                                                                                                                      356
                       536
                                                                                                                                                                           254
                                                                                                                                                                                                297
                                                                                                                                                                                                                      201
                                                                                                                                                                                                                                                                                                                                                                        ΑŦ
   487
                                           427
                                                                                     368
                                                                                                                                308
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YDLLLEMLDAHRLHA-PTSRGGASVEETDQSHLATAGSTSSHS

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Best Local S
Matches 24
                                                                                                                                                                                                                                                                                             DNA_BIND
                                                                                                                                                                                                                                                                                                                                                           MGD; MGI
PROSITE;
                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1991 (REL.
01-FEB-1991 (REL.
01-NOV-1997 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESTR_MOUSE
P19785;
                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                     TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WHITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=UTERUS;
MEDLINE; 91042558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESTROGEN RECEPTOR (ER) (ESTRADIOL RECEPTOR) ESR1 OR ESR OR ESTR OR ESTRA.
                                                                                                                                                                                                                                                                                                                                   ZINC-FINGER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUTHERIA;
243
                        287
                                                187
                                                                      227
                                                                                                131
                                                                                                                     167
                                                                                                                                                                       108
                                                                                                                                               73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE 1 THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES. SUBUNIT: HOMODIMER. SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPLEX APPEARS TO RECOGNIZE DISCRETE DNA SEQUENCES UPSTREAM OF TRANSCRIPTIONAL START SITES.
SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMA:
A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
IN THE ABSENCE OF LIGAND, STEROID HORMONE RECEPTORS ARE THOUGHT
TO BE WEAKLY ASSOCIATED WITH NUCLEAR COMPONENTS; HORMONE BINDING
GREATLY INCREASES RECEPTOR AFFINITY. THE HORMONE-RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEAR HORMONE RECEPTORS.; M38651; G193180; -.
                                                                                                                                                                                                                                                                                                                                           MGI:109348; ESTRA.
ITE; PS00031; NUCLEAR_RECEPTOR;
PTOR; TRANSCRIPTION REGULATION;
                                              ERLSSSNEKGNMIMESAKETRYCAVCNDYASGYHYGVWSCEGCKAFFKRSIQGHNDYMCP 226
                                                                                                                                                                    SPSPLMLLHPPPQLSPFLHPHGQQVPYYLENEPSAY-AVRDTGPPAFYRSNSDNRRQNGR 166
                                                                                                                                                                                                                                                                                                                                                                                                          A40061
GKAKRSGG--HAPRV-RELLLD--ALS--PEQLVLTLLEAEPPHVLIS-RPSAPFTEASM
                                                                                             NR-CASPVTGP---GSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICP
                                                                                                                                             TTSPNVLWPTPGHLSP-LVVHRQLSHLYAEPQKSPWCEARSLEHTLPVNRETLKRKVSG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENDOCRINOL. 1:735-744(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YDLLLEMLNAHVLRGCKSSITGSECSPAEDSK-SKEGSQNPQS 529
                     SGDMRAANLWPSPLVIKHTKKNSPALSLTADQMVSALLDAEPPMIYSEYDPSRPFSEASM
                                                                                                                                                                                                                                                                                                                                                                                                P06536;
                                                                                                                                                                                                                                                                                                                                                                                                          M38651; G19318
140061; A40061.
                                                                                                                                                                                              246;
                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                               599
                                                                                                                                                                                                                                                                      189
189
225
255
                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                   STEROID-BINDING
                                                                                                                                                                                                                                               ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17, CREATED)
17, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                          42.8%;
51.7%;
                                                                                                                                                                                                                                                            188
254
209
249
599
                                                                                                                                                                                                                                               66955 MW;
                                                                                                                                                                                              106;
                                                                                                                                                                                                                                                                    MODULATING.
C4-TYPE ZINC FINGERS
C4-TYPE.
C4-TYPE.
C4-TYPE.
STEROID-BINDING.
                                                                                                                                                                                                          Score 1669; DB 1;
Pred. No. 0.00e+00;
                                                                                                                                                                                                                                                            POLY-ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                             6ED9EADB CRC32;
                                                                                                                                                                                              Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAM J.,
                                                                                                                                                                                                                                                                                                                                             DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A MODULATING N-TERMINAL DOMAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PARKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ĄĄ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Χ.,
                                                                                                                                                                                                                   Length 599;
                                                                                                                                                                                                                                                                                                                                              NUCLEAR PROTEIN;
                                                                                                                                                                                             Indels 20;
                                                                                                                                                                                                                                                                                                          (OWT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HORMONE BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INVOLVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CELLULAR
                                                                                                                                                                                            Gaps
                     346
                                                                                                                                             130
                                              242
                                                                     286
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SALAN 
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DNA_BIND
ZN_FING
ZN_FING
DOMAIN
DOMAIN
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBMITTED (JUN-1991) TO EMBL/GENBANK/DDBJ DATA BANKS.
-- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE ITHE REGULATION OF BURKRYOTIC GENE EXPRESSION AND AFFECT PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
                                                                                                                                                                                                                                                                                   HSSP;
                                                                                                                                                                                                                                                                                                    EMBL; Y00102; G56111; -. EMBL; X61098; G56121; -. EMBL; S07379; S07379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 87174780. KOIKE S., SAKAI M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1988 (REL.
01-JAN-1988 (REL.
01-NOV-1997 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KOIKE S., SAKAI M. NUCLEIC ACIDS RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-WISTAR;
                                                                                                                                                                     DOMAIN
                                                                                                                                                                                           ZINC-FINGER;
                                                                                                                                                                                                                 RECEPTOR:
                                                                                                                                                                                                                                                             TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAGGI A.M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-SPRAGUE-DAWLEY; TISSUE-UTERUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBMITTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MURAMATSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RATTUS NORVEGICUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESTROGEN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P06211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESTR_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              474
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                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN. A DNA-BINDING DOMAIN, STEROID HORMONE RECEPTORS ARE THOUGHT TO BE WEAKLY ASSOCIATED WITH NUCLEAR COMPONENTS; HORMONE BINDING GREATLY INCREASES RECEPTOR AFFINITY. THE HORMONE-RECEPTOR COMPLEX APPEARS TO RECOGNIZE DISCRETE DNA SEQUENCES UPSTREAM OF TRANSCRIPTIONAL START SITES.

SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC
                                                                                                                                                                                                                                                                                                                                                                          NUCLEAR HORMONE RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSTLKSLEEKDHIHRVLDKITDTLIHLMAKAGLTLQQQHRRLAQLLLILSHIRHMSNKGM
::| ::|::|::|::|::|::|:|:|:||
TATQDA-DSSRKLAHLLNAVTDALVWVIAKSGISSQQQSMRLANLLMLLSHVRHASNKGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OR ESR OR ESTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EHLLNMKCKNVVPVYDLLLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSQNPQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFAPNILLDRNQGKCYEGMYEIFDMLLATSSRFRMMNLQGEEFYCLKSIILLNSGYYTFL 466
:|||:||:||||:||||:||:||
IFAPDLYLDRDEGKCYEGILEIFDMLLATTSRFRELKLQHKEYLCYKAMILLNSSMYPLV 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EHLYNMKCKNVVPLYDLLLEMLDAHRLHAPASRMGVPPEEPSQTQLATTSSTSAHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MMSLTKLADKELVHMISWAKKIPGFVELSLFDQVRLLESCWMEVLMMGLMWRSIDHPGKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGLITNLADRELVHMINWAKRVPGFGDLNLHDQVHLLECAWLEILMIGLVWRSMEHPGKL
                                                                                                                                                                                                                                                                                   P06536; 1GDC
                                                                                                                                                                                                            PS00031; NUCLEAR_RECEPTOR; TRANSCRIPTION REGULATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RODENTIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METAZOA;
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06, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE)
(ER) (ESTRADIOL RECEPTOR).
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67030
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  WW;
                   C4-TYPE ZINC FIN
C4-TYPE.
C4-TYPE.
STEROID-BINDING.
STEROID-BINDING.
POLY-ALA.
N -> T (IN REF.
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-> T (IN REF. 3
4CCC59B2 CRC32;
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Query Best I

Local Match

Similarity

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ESTR_PIG STAN
Q29040;
01-NOV-1997 (REL. 3
01-NOV-1997 (REL. 3
01-NOV-1997 (REL. 3
                                                                                                                                                                                                                   BOEKENKAMP D., JUNGBLUT P.W., THOLE H.H.;

MOL. CELL. ENDOCRINOL. 104:163-172(1994).

-i- FUNCTION: THE STEROID HORMORES AND THEIR RECEPTORS ARE 1

THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT

THE REGULATION AND DIFFERENTIATION IN TARGET TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                  ESTROGEN RECEPTOR
ESR1 OR ESR.
SUS SCROFA (PIG).
               NUCLEAR HORMONE RECEPTORS.
EMBL; Z37167; G587555; -
PROSITE; PS00031; NUCLEAR RECEPTOR;
RECEPTOR; TRANSCRIPTION REGULATION;
                                                                                                                                                 -
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                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; METAZOA;
EUTHERIA; ARTIODACTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131
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                                                                       SUBUNIT: HOMODIMER.

SUBCELLULAR LOCATION: NUCLEAR.

SUBCELLULAR LOCATION: NUCLEAR.

SUBCELLULAR LOCATION: NUCLEAR.

BOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOI DOMAIN.

A DNA-BINDING DOMAIN AND A C-TERMINAL STERCID-BINDING DOMAIN.

IN THE ABSENCE OF LIGAND, STEROID HORMONE RECEPTORS ARE THOUGH THE HASENCE OF LIGAND, STEROID HORMONE RECEPTORS APPINITY. THE HORMONE-RECEPTOR GREATLY INCREASES RECEPTOR AFFINITY. THE HORMONE-RECEPTOR COMPLEX APPEARS TO RECOGNIZE DISCRETE DNA SEQUENCES UPSTREAM TRANSCRIPTIONAL START SITES.

TRANSCRIPTIONAL START SITES.

SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTSPNVLWPTPGHLSP-LVVHRQLSHLYAEPQKSPWCEARSLEHTLPVNRETLKRKVSG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPSPLMLLHPPPHVSPFLHPHGHQVPYYLENEPSAY-AVRDTGPPAFYRSNSDNRRQNGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERLSSSSEKGNMIMESAKETRYCAVCNDYASGYHYGVWSCEGCKAFFKRSIQGHNDYMCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATQDA-DSSRKLAHLLNAVTDALVWVIAKSGISSQQQSMRLANLLMLLSHVRHASNKGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGLLTNLADRELVHMINWAKRVPGFGDLNLHDQVHLLECAWLEILMIGLVWRSMEHPGKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A--KRSGG--HAPRV-RELLLD--ALS--PEQLVLTLLEAEPPHVLIS-RPSAPFTEASM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATNQCTIDKNRRKSCQACRLRKCYEVGMMKGGIRKDRRGGRMLKHKRQRDDLEGRNEMGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NR-CASPVTGP---GSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EHLYNMKCKNVVPLYDLLLEMLDAHRLHAPASRMGVPPEEPSQSQLITTSSTSAHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSTLKSLEEKDHIHRVLDKINDTLIHLMAKAGLTLQQQHRRLAQLLLILSHIRHMSNKGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MMSLTKLADKELVHMISWAKKIPGFVELSLFDQVRLLESCWMEVLMMGLMWRSIDHPGKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGDMRAANLWPSPLVIKHTKKNSPALSLTADQMVSALLDAEPPLIYSEYDPSRPFSEASM
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larity 51.1%;
Conservative
ANSCRIPTION REGULATION; STEROID-BINDING.
                                                                                                                                                                                                                                                                                                                         N.A.,
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                                                                                                                                                                                                                                                                                                                                                                     CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                            CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
( ESTRADIOL RECEPTOR).
                                                                                                                                                                                                                                                                                                                            PARTIAL SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                     VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                  DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        595
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                                                                                                                      PONENTS; HORMONE BINDING HORMONE-RECEPTOR
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                   NUCLEAR
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DNA_BIND
ZN_FING
ZN_FING
DOMAIN
DOMAIN
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P50240;
01-OCT-1996
01-NOV-1997
01-NOV-1997
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                                                                        TISSUE=BLOOD
MEDLINE; 962
                                                                                                             MEDLINE; 97120581.
TAN N.S., LAM T.J., DII
MOL. CELL. ENDOCRINOL.
 + + +
                                                                                          SEQUENCE OF 270-583
                                                                                                                                                                   EUKARYOTA; METAZOA;
                                                                                                                                                                            OREOCHROMIS
                                                                                                                                                                                               ESTROGEN
                                                                                                                                        SEQUENCE FROM
                                                                                                                                                           OSTEICHTHYES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 SPSPLVLLHPPPQLSPFLHPHGQQVPYYLENEPSGY-AVREAGPPAFYRPNSDNRRQGGR 162
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N., LAM T., DING J.;
SEQ. 5:359-370(1995).
SEQ. 5:359-370(1995).
FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE:
THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT
PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
SUBUNIT: HOMODIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR.
DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTSPNVLWPTPGHLSP-LVVHRQLSHLYAEPQKSPWCEARSLEHTLPVNRETLKRKVSG-
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EHLLNMKCKNVVPVYDLLLEMLNAHVLRG
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(REL.
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                                                                                                                                                          TAZOA; CHORDATA;
ACTINOPTERYGII;
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                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                             34, CREATED)
35, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDATE
(ER) (ESTRADIOL RECEPTOR).
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250
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DL. 123:149-161(1996).
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C4-TYPE ZINC FINGERS (TWO).
C4-TYPE.
C4-TYPE.
HINGE.
STEROID-BINDING.
W; E50DF7AC CRC32;
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Pred.
97; M
                                                                                                                                                          VERTEBRATA;
PERCIFORMES
                                                                                                                                                                                                                                            PRT;
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No. 0.
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  N-TERMINAL
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                                       T CELLULAR
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  DOMAIN,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; X93558; E256017; JOINED.; X93559; E256017; JOINED.; X93559; E256017; JOINED.; X93560; E256017; JOINED.; Z46666; E256017; JOINED.; Z46666; E256017; JOINED.; Z46668; E256017; JOINED.; Z46668; E256017; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A DNA-BINDING
SIMILARITY: TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEAR HORMONE
                                                                                     QQQSRRQAQLLLLLSHIRHMSNKGMEHLYSMKCKNKVPLYDLLLEMLDAHRIHRPVKPS
                                                                                                                         LKLKPEEFVCLKAIILLNSGAFSFCTGTMEPLHDSVAVQHMLDTITDALIFHISHFGCSA 451
                                                                                                                                                    EGCKAFFKRSIQGHNDYMCPATNQCTIDKNRRKSCQACRLRKCYEVGMMKGGMRKDR-G-
                                                                                                                                                                                                                                                                                                                                                              YSAPLDAHG-PLSDGSLQS-LGSGPTSPLVFVPSSPRLSPFM-HPP-SHHYLETTSTP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; 246669; E256017; ; 246665; E212276; ; 246666; E212276; ; 2466667; E212276; ;
                                                                                                                LKLQHKEYLCVKAMILLNSSMYPLVTATQDA-DSSRKLAHLLNAVTDALVWVIAKSGISS
                                                                                                                                                                                                                                            RVLRREKHGPAQRQTSQNLPTHKASPQDGRKRAMSSSSTSGPGGRSSL-NNMPPDQVLLL
                                                                                                                                                                                                                                                                      EGCKAFFKRSIQGHNDYICPATNQCTIDKNRKSCQACRLRKCYEVGMVKCGSRRERCGY
                                                                                                                                                                                                                                                                                                           EARSLEHTLPVNRETLKRK-V-SGNRCASPVTGPGSKRDAHFCAVCSDYASGYHYGVWSC
                                                                                                                                                                                                                                                                                                                                VYRSSHQPVPREDQCGTRDEAYSVGELGAGAGGFEITKNTRFCAVCSDYASGYHYGVWSC
                                                                                                                                                                                                                                                                                                                                                   YSPAVMNYSIPSNYTNLEGGPGRQTTSPNYLWPTPGHLSPLVVHRQLSHLYAEPQKSPWC
                                                                            QQQSMRLANLLMLLSHVRHASNKGMEHLLNMKCKNVVPVYDLLLEMLNAH-VLRGCKSS
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246669; E212276;
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                                      STANDARD;
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CREATED)
LAST SEQUENCE UI
LAST ANNOTATION
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Pred. No. 0.00e+00;
90; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                      C4-TYPE ZINC FINC
C4-TYPE.
C4-TYPE.
STEROID-BINDING
POLY-LEU.
POLY-LEU.
POLY-GIY.
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            UPDATE )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA-BINDING; NUCLEAR
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ZINC FINGERS (TWO).
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SEQUENCE
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-!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS A
THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFF
PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORYZIAS LATIPES (MEDAKA FISH).
EUKARYOTA; METAZOA; CHORDATA;
OSTEICHTHYES; ACTINOPTERYGII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESTROGEN RECEPTOR (ER) (ESTRADIOL RECEPTOR).
ESR.
ORVZIAS LATIPES (MEDAKA FISH).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZINC-FINGER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00031; NUCLEAR_RECEPTOR; RECEPTOR; TRANSCRIPTION REGULATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERM A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING -i- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RENUCLEAR HORMONE RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OKADA H
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 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: NUCLEAR
                                                                                                                                  PAMTEYSPAVMNYSIPSNVTNLEGGPGRQTTSPNVLWPTPGHLSPLVVHRQLSHLYAEPQ
GVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCYEVGMVKCGSRR
                                                                                                                                                                                                                GVWSCEGCKAFFKRSIQGHNDYMCPAINQCTIDRNRRKSCQACRLRKCYEVGMMKGGVRK
                                                                                                                                                                                                                                              KSPWCEARSLEHTLPVNRETLKRKVS-GNRCASPVTGPGSK-RDAHFCAVCSDYASGYHY
                                                                                                                                                                                                                                                                                                  SSTGYYSAPLETNGPPSE-GSLQS-LGSGPTSPLVFVPSSPRLSPFM-HPP-SHHYLETT:::||:::||:::|||::||||
                                                                                DQVRLLESCWMEVLMMGLMWRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFDMLLATTS
                                                                                         DQVLLLESSWLEVLMIGLIWRSIHCPGKLIFAQDLILDRNEGDCVEGMTEIFDMLLATAS
                                                                                                                       LVLTLLEAEPPHVLISRPS-A-PFTEASMMSLTKLADKELVHMISWAKKIPGFVELSLF
                                                                                                                                                                                                                                                          STPYYRSSHQGASREDQCGSREDTCSLGELGAGAGAGGFEMAKDTRFCAVCSDYASGYHY 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D28954; G602326;
                                                                                                                                                                                                                                                                                                                                 h 40.8%;
Similarity 52.8%;
252; Conservative
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141
177
177
207
254
275
466
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                                                                                                                                                                                                                                                                                                                               Score 1591; DB 1;
Pred. No. 0.00e+00;
93; Mismatches 108;
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POLY-LEU.
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C4-TYPE.
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D9FE40D0
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DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZINC
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501
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Best Local
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01-APR-1990 (REL. 1
01-APR-1993 (REL. 2
01-NOV-1997 (REL. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE; 910
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ZN_FING
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                       143
                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                   ZINC-FINGER;
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                                                                                                                                                                                                                 145
                        368
                                               381
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 441
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FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: TO OTHER MEMBERS NUCLEAR HORMONE RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPLEX APPEARS TO RECOGNIZE DISCRETE DNA SEQUENCES UPSTREAM TRANSCRIPTIONAL START SITES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TO BE WEAKLY ASSOCIATED WITH NUCLEAR COMPONENTS; HORMONE GREATLY INCREASES RECEPTOR AFFINITY. THE HORMONE-RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                     A37197; A37197.
A40070; A40070.
; P06536; IGDC.
                                                                                                                                                                                                                            ETRYCAVCSDFASGYHYGVWSCEGCKAFFKRSIQGHNDYMCPATNQCTMDRNRRKSCQAC
                                                                                                                                     SINGGGGWRGPRITMPPEQVLFLLQGQTP-ALCSRQKVARPYTEVTMMTLLTSMADKELV 320
                                                                                                                                                                                                                 DAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQAC
                      KCVEGILEIFDMLLATISRFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDA-DSSRKL
                                                                                HMIAWAKKYPGFQELSLHDQVQLLESSWLEVLMIGLIWRSIHCPGKLIFAQDLILDRSEG
                                                                                                                    RVREL--LLDA-LS-PEQLVLTLLEAEPPHVLISRPS-A-PFTEASMMMSLTKLADKELV
                                                                                                                                                                                RLRKCYEVGMVKGGLRKDRGG-RVLRKDKRYCGPAGDREKPTVTWSTGQRPQDGGRNSSS
ESMLDNITDALIHHISHSGASVQQQPRRQAQLLLLLSHIRHMSNKGMEHLYSIKCKNKVP
                                               DCVEGMAEIFDMLLATVSRFGMLKLKPEEFVCLKAIILLNPGAFSFCSNSVESLHNSSAV
                                                                      HMISWAKKIPGFVELSLFDQVRLLESCWMEVLMMGLMWRSIDHPGKLIFAPDLVLDRDEG
                                                                                                                                                                   RLRKCYEVGMVKCGSRRERCGYRLVRRQ-R---SA-D-EQLHCA-GKAKRS--GGH--AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN.

DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.

N THE ABSENCE OF LIGAND, STEROID HORMONE RECEPTORS ARE THOUGHT
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F., LE GAC F., L
LL. ENDOCRINOL.
                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                           PS00031; NUCLEAR_RECEPTOR; 1.; TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR
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183
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25, 1
35, 1
(ER)
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167
207
574
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                                                                                                                                                                                                                                                                                                             62872 MW;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LE GOFF P., VALOTAIRE . 71:195-204(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N.A.
                                                                                                                                                                                                                                                               Score
Pred.
78; M
                                                                                                                                                                                                                                                                                                                        C4-TYPE ZINC FING
C4-TYPE.
C4-TYPE.
STEROID-BINDING
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P50242;
01-OCT-1996
01-OCT-1996
01-NOV-1997
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SUBMITTED (JUL-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.

-!- FUNCTION: THE STEROID HORNONES AND THEIR RECEPTORS ARE INVOLV
THE REGULATION OF EUKARYCTIC GENE EXPRESSION AND AFFECT CELLU
PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.

-!- SUBUNIT: HOMODIMER (BY SIMILARITY).

-!- SUBCULTLIAR LOCATION: NUCLEARITY).

-!- SUBCELLULAR LOCATION: NUCLEARITY.

-!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DO
A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID/BINDING DOMAIN.

-!- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC
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EUKARYOTA; METAZOA; CHORDATA;
OSTEICHTHYES; ACTINOPTERYGII;
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PROSITE; PS00031; NUCLEAR_RECEPTOR;
RECEPTOR; TRANSCRIPTION REGULATION;
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KLAHLLNAVTDALVWVIAKSGISSQQQSMRLANLLMLLSHVRHASNKGMEHLLNMKCKNV
                                           AVESMLDNITDALIHHISHSGASVQQQPRRQVQLLLLLSHIRHMSNKGMEHLYSIKCKNK
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34, LAST SEQUENCE UPDATE)
35, LAST ANNOTATION UPDAT
(ER) (ESTRADIOL RECEPTOR)
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C4-TYPE.
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GIGUERE V., YANG N., SEGUI P., EVANS
NATURE 331:91-94(1988).
-i- SUBCELLULAR LOCATION: NUCLEAR (P
-i- SIMILARITY: TO OTHER MEMBERS OF
NUCLEAR HORMONE RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P11475;
01-OCT-1989 (REL. 12, CREATED)
01-OCT-1989 (REL. 12, LAST SEQ
01-OCT-1994 (REL. 30, LAST ANN
STEROID HORMONE RECEPTOR ERR2.
                    ERRI_HUMAN STANDARD; PRT; 521 AA P11474; 01-0CT-1989 (REL. 12, CREATED) 01-0CT-1989 (REL. 12, LAST SEQUENCE UPDATE) 01-0CT-1994 (REL. 30, LAST ANNOTATION UPDAT STEROID HORMONE RECEPTOR ERRI.
    ERR1.
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TRANSCRIPTION REGULATION; DNA-BINDING;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.7%;
larity 39.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12, CREATED)
12, LAST SEQUENCE UPDATE)
30, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168
123
163
48287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHORDATA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 807; DB 1; Lo
Pred. No. 9.34e-162;
84; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C4-TYPE ZINC
C4-TYPE.
C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERTEBRATA; TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              673BF88F
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M
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                                              UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22;
                                                                                                                                                                                                                         499
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Best Local
                                                                                                                                                                                                   PRGR_SHEEP
Q28590;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA_BIND
ZN_FING
ZN_FING
SEQUENCE
SEQUENCE FROM N.A.
STRAIN-ROMANOV; TISSUE-UTERUS;
STRAIN-ROMANOV; TISSUE-UTERUS;
MADIGOU T., TIFFOCHE C., LE GAL F., PELLETIER J., THIEULANT
SUBMITTED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
-!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE I
THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT
PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA;
EUTHERIA; PRIMATES.
[1]
                                                                                                                                           OVIS ARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                         PGR
                                                                                                                                                                              01-NOV-1997
01-NOV-1997
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NATURE 331:91-94(1988)
                                                                                                                                                                   PROGESTERONE
                                                                                                                    EUTHERIA;
                                                                                                                                  EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RECEPTOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
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                                                                                                                                                                                                                                                                         445 GISSQQQSMRLANLLMLLSHVRHASNKGMEHLLNMKCKNVVPVYDLLLEMLNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 RICLYCGDVASGYHYGVASCEACKAFFKRTIQGSIEYSCPASNECEITKRRRKACQACRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEAN NO. 18609; -.
BL; X51416; G36609; -.
IR; A29345; A29345.
3SP; P06536; 1GDC.
ROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
ROSITE; PS00031; NUCLEAR_RECEPTOR; D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: NUCLEAR SIMILARITY: TO OTHER MEMBERS (
                                                                                                                                                                                                                                                                                                 GPGGGAERRRAGRLLLTLPLLRQTAGKVLAHFYGVKLEGKVPMHKLFLEMLEA
                                                                                                                                                                                                                                                                                                                                      RRLQALRLEREEYVLLKALALANSDSVHIEDEPRLWSSCEKLLH--EAL---LEYEAGRA
                                                                                                                                                                                                                                                                                                                                                                                     SDQMSVLQSVWMEVLVLGVAQRSLPLQDELAFAEDLVLD-EEGARAAGLGELGAALLQLV 410
                                                                                                                                                                                                                                                                                                                                                                                                                                   RKCYEVGMVKCGSRRERC-GYRLVRRQRSADEQLHCAGKAKRSGGHAPRVRELLLDALSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRL
                                                                                                                                                                                                                                                                                                                         SRFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDADSSRKLAHLLNAVTDALVWVIAKS
                                                                                                                                                                                                                                                                                                                                                                      FDQVRLLESCWMEVLMMGLMWRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFDMLLATT
                                                                                                                                                                                                                                                                                                                                                                                                                      EQLVLTLLEAEPPHVL-ISRPSAPFTEASMMMSLTKLADKELVHMISWAKKIPGFVELSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TKCLRVGMLKEGVRLDRVRGGRQKYKRRPEVDPLPFPG-P-FPAGPLAVAGGPRKTAAPV 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88122546
                                                                                                                   S (SHEEP).; METAZOA; CHORDATA; ARTIODACTYLA.
                                                                                                                                                                  7 (REL. 35, CREATED)
7 (REL. 35, LAST SEQU
7 (REL. 35, LAST ANNO
NE RECEPTOR (PR) (FRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176
176
212
521 AA;
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                                                                                                                                                                                                                            STANDARD;
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196
236
55742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW;
                                                                                                                                                                SEQUENCE UP
ANNOTATION
FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 800; 1
Pred. No. 5.;
74; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C4-TYPE.
1; E2D723EA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C4-TYPE ZINC C4-TYPE.
                                                                                                                               VERTEBRATA;
                                                                                                                                                                                                                            PRT;
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DF THE STEROID/THYROID/RETINOIC
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DNA-BINDING;
                                                                                                                                                                                          UPDATE)
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                                                                                                                                                                                                                           377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Le
5.20e-160;
ches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRC32;
 MODULATING N-TERMINAL DOMAIN
                                                                                                                                                                                                                           æ
                                                                                                                               TETRAPODA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FINGERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                               MAMMALIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                   INVOLVED :
                                                                                                                                                                                                                                                                           497
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                         Q00175;
01-DEC-1992 (REL. 24, C
01-DEC-1992 (REL. 24, I
01-NOV-1997 (REL. 35, I
PROCESTERONE RECEPTOR (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA_BIND
ZN_FING
ZN_FING
DOMAIN
                             HAGIHARÁ K., WÜ-PENG X.S., FUNABASHI T., KATO J., PFAFF D.W.;
BIOCHEM. BIOPHYS. RES. COMMUN. 205:1093-1101(1994).

-i- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
THE REGULATION OF EUGARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.

-i- SUBCELLULAR LOCATION: NUCLEAR.

-i- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN.
A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
-i- SIMILARITY: TO OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC
                                                                                                                                                                                         MEDLINE;
SCHOTT D.
EMBL;
                                                                                                                                           SEQUENCE OF 1-9
STRAIN=129/SV;
                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 91299759.
                                                                                                                                                                                                                                                        PGR
MUS
                                                                                                                                                                            BIOCHEMISTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZINC-FINGER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00031; NUCLEAR_RECEPTOR; RECEPTOR; TRANSCRIPTION REGULATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                   MEDLINE;
                                                                                                                                                                                                                                  EUTHERIA;
                                                                                                                                                                                                                                           EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                  PRGR_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                       OR PK.
MUSCULUS (MOUSE).
MUSCULUS (MOUSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A DNA-BINDING I
SIMILARITY: TO
                      NUCLEAR HORMONE RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEAR HORMONE RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                              LATTSRFRELKLOHKEYLCVKAMILLNS-SMYPLVTATQ-DADSSRKLAHLLNAV 433
                                                                                                                                                                                                                                                                                                                                                                                                                                       HIDDQITLIQYSWMSLMVFGLGWRSYKHGSGQMLYFAPDLILNEQRMK-ESSFYSLCLTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KCCQAGMVL-GGRKFK-KFNKVRVMRTLDAVALPQPVGIPNESQALSQRITFSPSQDLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ICLICGDEASGCHYGVLTCGSCKVFFKRAMEGQHNYLCAGRNDCIVDKFRRKNCPACRLR
                                                                                                                                                                                                                                                                                                                                                                                                   WQIPQEFVKLQVSQEEFLCMKVLLLLNTIPLEGLRSQNQFEEMRSSYITQLIKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPEQLVLTLLEAEPPHVLISRPSA-PFTEASMMSLTKLADKELVHMISWAKKIPGFVEL
 M68915;
U12644;
                                                                                                                                                                                                                                                                                                                                                                                                                         SLFDQVRLLESCWMEVLMMGLMWRSIDH-PGKLI-FAPDLVLDRDEGKCVEGILEIFDML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IP-PLINLLMSIEPDMYYAGHDNSKPDTSSSLLTSLNQLGERQLLSVVKWSKSLPGFRNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KCYEVGMVKCGSRRERCGYRLVRRQRSADE-QL-HCAGKAKRSGGHAPRVR-ELLLD-AL
                                                                                                                                                                                       D.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266555
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102; Conser
                                                                                                                                 95100931.
                                                                                                                                                                                                                                  RODENTIA.
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18
18
54
128
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larity 34.6%;
Conservative
                                                                                                                                                                            SHYAMALA G.,
30:7014-7020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STEROID-BINDING
G200472;
G639917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                       FROM
                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                        24, CREATED)
24, LAST SEQUENCE 35, LAST ANNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15
83
38
78
>377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN O OTHER MEMBERS OF THE STEROID/THYROID/RETINOIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42840
                                                                                                                                                       N.A.
                                                                                                                                                                                                                                                                             LAST
LAST
(PR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MW;
                                                                                                                                                                            (1991).
                                                                                                                                                                                       SCHNEIDER
                                                                                                                                                                                                                                                                                       SEQUENCE UPDATE)
ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 679; I
Pred. No. 5.2
82; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MODULATING, PRO-I
C4-TYPE ZINC FINC
C4-TYPE.
C4-TYPE.
STEROID-BINDING.
                                                                                                                                                                                                                                             VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6F0DD900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                      Ε.
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                                                                                                                                                                                                                                                                                                                                  923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Le
.25e-130;
.ches 98;
                                                                                                                                                                                       PARRY
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Best Local S
Matches 12
[2]
[SQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.

MEDLINE; 87184565.

MISRAHI M., ATGER M., D'AURIOL L., LOOSFELT H., MERLLL C.,

FILDLANSKY F., GUIOCHON-MANTEL A., GALIBERT F., MILGROM E.;

BIOCHEM. BIOPHYS. RES. COMMUN. 143:740-748(1987).

-!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR

THE REGULATION AND DIFFERENTIATION IN TARGET TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1988
01-AUG-1990
01-OCT-1996
                                                                                                                                                                                                                                                                 MEDLINE;
KASTNER I
CHAMBON I
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                                                                                                                                                                                                                                               EMBO J.
                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                   EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA;
                                                                                                                                                                                                                                                                                                                                                                                                        HOMO SAPIENS (HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROGESTERONE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A39596; A39596.
HSSP; P06536; 1GDC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; P06536; 1GDC.
MGI:97567; PGR.
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90228361.
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(REL. 15, LAST SEQUENCE UF
(REL. 34, LAST ANNOTATION
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NUCLEAR LOCALIZATION
; EEDFF41A CRC32;
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DNA-BINDING;
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EMBL; M15716; G189935; -.

PIR; A03245; ORHUP.

PIR; S09971; S09971.

HSSP; P06536; IGDC.
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P06186;
01-JAN-1988
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PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.

RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING; NI

RICC-FINGER; STEROID-BINDING; PHOSPHORYLATION; ALT

TINC-FINGER; STEROID-BINDING; PRO-BICH.
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                   PROGESTERONE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: NUCLEAR.

DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
A LITERNATIVE PRODUCTS: THERE ARE TWO FORMS OF THE PROGESTERONE
RECEPTOR: FORM A (THAT STARTS WITH MET-1) AND FORM B (THAT STARTS
WITH MET-165).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEAR HORMONE RECEPTORS.
                                                                                                                                                                                                                               LRQKGVVSSSQRFYQLTKLLDNLHDLVKQ 886
                                                                                                                                                                                                                                                                                       WQIPQEFVKLQVSQEEFLCMKVLLLLNTIPLEGLRSQTQ-FEEMRS-SYI-RELIKAIG-
                                                                                                                                                                                                                                                                                                                                             SLFDQVRLLESCWMEVLMMGLMWRSIDH-PGKLI-FAPDLVLDRDEGKCVEGILEIFDML
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E RECEPTOR
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33.4%;
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LAST SEQUENCE UI
LAST ANNOTATION
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C4-TYPE ZINC FINGERS (
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STEROID-BINDING.
STEROID-BINDING (BY CK
PHOSPHORYLATION (BY CK
PHOSPHORYLATION (BY CK
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Pred. No. 8.35e-127;
89; Mismatches 113;
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Best Local
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
EUTHERIA; LAGOMORPHA.
[1]
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HSSP, P06536; 1GDC
TRANSERC
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MEDITINE: 87067449.

LOOSFELT H., ATGER M., MISRAHI M., GUIOCHON-MANTEL A., M
LOOSFELT H., BENAROUS R., MILGROM E.;

PROC. NATL. ACAD. SCI. U.S.A. 83:9045-9049(1986).

-!- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS A
THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFF
PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
-!- SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSFAC; T00697; -.
PROSITE; PS00031; NUCLEAR_RECEPTOR;
RECEPTOR; TRANSCRIPTION REGULATION;
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                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                               DDQITLIQYSWMSLMVFGLGWRSYKHVSGQMLYFAPDLILNEQRMK-ESSFYSLCLTMWQ
KSGISSQQQSMRLANLL-MLLSHVRH
                                                TTSRFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDADSSRKLAHLLNAVTDALVWVIA
                                                                                              FDQVRLLESCWMEVLMMGLMWRSIDH-PGKLI-FAPDLVLDRDEGKCVEGILEIFDMLLA
                                                                                                                                                   EQUVLTLLEAEPPHYLISRPSA-PFTEASMMMSLTKLADKELVHMISWAKKIPGFVELSL
                                                                                                                                                                  -PLINLLMSIEPDVIYAGHDNTKPDTSSSLLTSLNQLGERQLLSVVKWSKSLPGFRNLHI
                                                                                                                                                                                                                FCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLR
                      KGVVSSSQRFYQLTKLLDNLHDLVKQ
                                                                        IPQEFVKLQVSQEEFLCMKVLLLLNT-I-PLEGLRSQSQFEEMRSSYIRELIKAIG-LRQ
                                                                                                                                                                                                    KCYEVGMVKCGSRRERCGYRLVRRQRSADE-QL-HCAGKAKRSGGHAPRVRELLLDALSP
                                                                                                                                                                                                                                                                                                        106;
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C4-TYPE.
C4-TYPE.
STEROID-BINDING.
NUCLEAR LOCALIZATION S
W; EE133E86 CRC32;
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91; N
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Pred. No. 8.05e-126;
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                       883
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Nov 3 04:56:49 1998; MasPar time 74.31 Seconds 1058.292 Million cell updates/sec

Tabular output not generated.

Title:

>US-08-906-365-1 (1-1686) from US08906365.seq 1686

Description:
Perfect Score:
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Comp: 1 cagccattatacttgcccac......agaacccacagtctcagtga 1686 gtcggtaatatgaacgggtg......tcttgggtgtcagagtcact

Scoring table: TABLE default Gap 6

Nmatch STD: Dbase 0; Query 0

Searched: 88822 seqs, 23323279 bases x

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

n-issued 1:5_COMB 2:PCT9_COMB 3:backfiles1

Statistics: Mean 9.055; Variance 4.480; scale 2.021

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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                                                                                                                                                                                                                                  Patent No. 5650298
GENERAL INFORMATION:
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                                                                                                                      TITLE OF INVENTION: Tight Control of Gene Expression TITLE OF INVENTION: Cells by Tetracycline-responsive NUMBER OF SEQUENCES: 10
                                                                                                                                                                     APPLICANT: Salfeld, Joche APPLICANT: Voss, Jeffrey
                                                                                                                                                                                                   APPLICANT:
    COMPUTER
                                                                                                        CORRESPONDENCE ADDRESS:
                              STREET: 60 Sta
CITY: Boston
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                                                                                           ADDRESSEE:
                   02109-1875
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Application US/08260452
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larity 66.7%;
Conservative
                                                Massachusetts
                                                                             60 State Street
                                                                                                                                                                                      Bujard, Hermann
Salfeld, Jochen
                                                                                                                                                                                                                Gossen, Manfred
                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                             Lahive & Cockfield
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Pred. No. 2.47e-138;
0; Mismatches 209;
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Best Local (
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                                   2011
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TELEFAX: (617) 227-5941
INFORMATION FOR EGO ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4963 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 11.7%;
Local Similarity 66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BBI-013CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227,7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/0
ATTORNEY/AGENT INFORMATION:
NAME: Giulio A. DeConti,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy COMPUTER: IBM PC COMPUTER: OPERATING SYSTEM: PC SOFTWARE: ASCII text
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCCACCTTCTAGAATGTGCCTGGCGTAGAGATCCTGATGATTGGTCTCGTCTGGCGCTCC
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                                                                              ACCCTGCAGCAGCAGCAGCGGCGGGCGGGCCCAGCTCCTCCTCATCCTCTCCCACATCAGG
                                                                                                                                                                                                                   TCTGGAGTGTACACATTTCTGTCCAGCACCCTGAAGTCTCTGGAAGAGAAGAAGCACCATATC
                                                                                                                                                                                                                                                                     CGCATGATGAATCTGCAGGGAGGAGGAGTTTGTGTGCCTCAAATCTATTATTTTGCTTAAT
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    catgcgagtaacaagggcatggaacatctgctcaacatgaagtgcaaaaatgtggtccca
                                   CACATGAGTAACAAAGGCATGGAGCATCTGTACAGCATGAAGTGCAAGAACGTGGTGCCC
                                                            tcacttg--ctgaacgccgtgaccgatgctttggtttgggtgattgccaagagcggcatc
                                                                                                                                                          cgagagttaaaactccaacacaaagaatatctctgtgtcaaggccatgatcctgctcaat
                                                                                                                                                                                                                                                                                                               aaatgcgtagaaggaattctggaaatctttgacatgctcctggcaactacttcaaggttt
                                                                                                                                                                                                                                                                                                                                                                                                                                       gtgcggctcttggagagctgttggatggaggtgttaatgatggggctgatgtggcgctca
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SYSTEM: PC-DOS/MS-DOS
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31,503
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Pred. No. 2.47e-138;
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Sequence 1, Applic
Patent No. 5550024
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                                                                                                                                                                                        TELEFAX: 515-288-1338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3460 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07, FILING DATE: 19-APR-1991
ATTORNEY/AGENT INFORMATION: NAME: Nebel, Heidi S. REGISTRATION NUMBER: 37,7;
                                                                                  ANTI-SENSE: NO
FEATURE: NO
FEATURE: MISC_feature
NAME/KEY: MISC_feature
LOCATION: 303.304
OTHER INFORMATION: /note
OTHER INFORMATION: undet
                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/961,819
FILING DATE: 19-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Relea
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O
FILING DATE: 26-SEP-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy
                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: BF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-288-3667
                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rothschild, Max F. APPLICANT: Tuggle, Christophe
           FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Genetic Markers for Pig Litter Size NUMBER OF SEQUENCES: 9
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                                LOCATION: 1197..11
OTHER INFORMATION:
OTHER INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                             STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Des Moines
                                                              NAME/KEY:
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Application US/08312312A
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Plastow, Graham S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tuggle, Christopher K. Jacobson, Carol D.
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1197..1198
exon
534..600
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                                                                                                                                                           DNA (genomic)
                                                                                    /note= "Gap in DNA sequence
undetermined length"
                                undetermined
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                                                                                                                                                                                                                                                                                                                          US 07/687,708
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                                   /note= "Gap in DNA sequence
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TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 6244 base pairs
                                                       2425
2485 GCATTGTTGATAAAATCCGCAGGAAAAACTGCCCGGCGTGTCGCCTTAGAAAGTGCTGTC 2544
                                                                                               2365 TCTGTGGGGATGAAGCATCAGGCTGTCATTATGGTGTCCTCACCTGTGGGAGCTGTAAGG 2424
                                                                                                                                                                                        STRANDEDNESS: both
TOPOLOGY: both
SEQUENCE 6244 BP; 1483 A; 1749 C; 1610 G; 1402 T; 0 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5464758 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Sequence 15,
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                              605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            680 tttttatcgattgtacactgatttgtagctggacaaatataatcattatgtcct 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     740 ttcaccattcccacttcgtaacacttccgaagtcggcaggcctggcagctcttgcgccgg 681
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/01
FILING DATE: 14-JUN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                          TCTTCTTTAAAAGGGCAATGGAAGGGCAGCATAACTATTTATGTGCTGGAAGAAATGACT 2484
                                                                                  tctgcagcgattacgcatcgggatatcactatggagtctggtcgtgtgaaggatgtaagg 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1100 New York Avenue, N.W
CITY: Washington
STATE: District of Columbia
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTCTTATCAATTGTGCACTGGTTGGTAGCTGGACACATGTAGTCATTATGTCCT 602
                           ccttttttaaaagaagcattcaaggacataatgattatatttgtccagctacaaatcagt 664
                                                                                                                                                                                                                                    TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                 NAME: Esmond, Robert W. REGISTRATION NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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Similarity 83.3%;
                                                                                                                                                   3.7%;
Similarity 66.3%;

    Application US/08076726
    Application US/08076726
    5464758

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1100 New York Avenue,
                                                                                                                                                                                                                                                                                                         (202)371-2600
(202)371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gossen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD; DNA; UNC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tight Control of Gene Expression in Eucaryotic Cells by Tetracycline-responsive Promoters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kessler, Goldstein & Fox
ork Avenue, N.W.
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                                                                                                                                                                                                                                                                                                                                                                 32,893
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Pred. No. 2.34e-35
                                                                                                                                                     Score 63; DB 1; I
Pred. No. 3.17e-29;
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                 2425 TCTTCTTTAAAAGGGCAATGGAAGGGCAGCATAACTATTTATGTGCTGGAAGAAATGACT 2484
                                           2365 TCTGTGGGGATGAAGCATCAGGCTGTCATTATGGTGTCCTCACCTGTGGGAGCTGTAAGG 2424
                                                                                                    CLONE: pUHD BGR3
SEQUENCE 6244 BP; 1483 A; 1749 C; 1610 G; 1402 T; 0 OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                  545
                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: BB TELECOMMUNICATION INFORMATION: 1617) 227-7400 TELEFAX: (617) 227-5941 INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076,327
ATTORNEY/ACENT INFORMATION:
NAME: Giulio A. DeConti, Jr.
REGISTRATION NUMBER: 31,503
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MEDIUM TYPE: Floppy of
COMPUTER: IBM PC com
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ADDRESSEE: Lahive & Cockfield
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                                                                                                                                                MOLECULE TYPE: |
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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                                                                                                            CLONE: PUHD BG
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SOFTWARE: ASCII text
                               tctgcagcgattacgcatcgggatatcactatggagtctggtcgtgtgaaggatgtaagg 604
                                                                                                                              ORGANISM: Human cytomegalovirus STRAIN: Towne (hCMV)
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                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
ccttttttaaaagaagcattcaaggacataatgattatatttgtccagctacaaatcagt
                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: doub
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Similarity 66.3%;

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                                                                           Score 63; DB 1;
Pred. No. 3.17e-29
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                               CLONE: I
SEQUENCE 7218
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                          IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA: APPLICATION NUMBER:
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APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
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8 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER
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26-AUG-1991
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Pred. No. 1.82e-28;
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INFORMATION FOR SEQ ID NO:
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APPLICANT:
                                                                                                                                                                                                                                      REFERENCE/DOSCRET NUMBER: 39,768
REFERENCE/DOCKET NUMBER: 304
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)83-4109
TELEFAX: 0703/63
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: EP 9:
FILING DATE: 26-AUG-1991
ATTORNEY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 44512 COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
TYPE: Floppy disk
                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
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                                                                                                                           TYPE: nucleic STRANDEDNESS: TOPOLOGY: line
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
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L8 BP; 1944 A
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                                                                                                                           linear
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                                                                     1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER
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                     3.6%;
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     200;
                     Score 61; DB 1;
Pred. No. 1.04e-27
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Query Match
Best Local Similarity
Matches 130; Conser
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Patent No. 5223606
APPLICANT: BLAUDIN DIERRE, DEJEAN, ANNE
TITLE OF INVENTION: S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN INAPPROPRIATELY EXPRESSED NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO:1:
Sequence 1, Application Sequence 1, Application Patent No. 5683885
                                                                                       US-08-759-873-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                              AGTGCTTTGAAGTGGGAATG
                                                                                                                                                                                                                                                 TAAGAACTGTGTTATTAATAAAAGTCACCAGGAATCGATGCCAATACTGTCGACTCCAGA
                                                                                                                                                                                                                                                                                                                   ATGTAAGGGCTTTTTCCGCAGAAGTATTCAGAAGAATATGATTTACACTTGTCACCGAGA 679
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FILING DATE: 17-DEC-1987
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ilarity 65.0%;
Conservative
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                                                                                       STANDARD;
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US/08759873
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                                                                                       DNA; UNC;
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Pred. No. 3.26e-23;
0; Mismatches 69
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Best Local :
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                                                                                                                 Sequence 1, Application US/08629939
Sequence 1, Application US/08629939
Patent No. 5645995
                                                                                                                                                                                                                                                                                                                                                                                      2001
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APPLICANT: Kiebac
                              GENERAL INFORMATION:
APPLICANT: Kieback, Dirk G.
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: RISK OF
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                               725
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TITLE OF INVENITY...

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS

STREET: 2100 Pennsylvania Avenue, N.W., Suite
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MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
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HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 3014 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                 AGGCTGGCATGGT 2073
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al Similarity 63.78;
123; Conservation
 ADDRESSEE:
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20037
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                                                                                                                                                                                                                                                                                                                                                                    Kieback,
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 SUGHRUE, MION,
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METHODS FOR DIAGNOSING AN INCREASED RISK
OF BREAST OR OVARIAN CANCER
                                METHODS FOR DIAGNOSING AN INCREASED RISK OF BREAST OR OVARIAN CANCER
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Pred. No. 9.86e-22;
0; Mismatches 70; Indels
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   MACPEAK & SEAS
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Best Local
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          Query Match
Best Local Similarity
Matches
                                                                                                              Patent No. 5260432.

Patent No. 5260432

APPLICANT: TAKAKU, FUMINARO; ISHIKAWA, TAKASHI; IMAWARI, MICHIO;
EVANS, RONALD M.; UMESONO, KAZUHIKO
TITLE OF INVENTION: HUMAN GAMMA RETINOIC ACID RECEPTOR DNA
NUMBER OF SEQUENCES: A
                                                                      SEQ ID NO:1:
                                                                                                                                                                                                                                                                                                                                                                                                                                          1881 TCTGTGGGGATGAAGCATCAGGCTGTCATTATGGTGTCCTTACCTGTGGGAAGCTGTAAGG 1940
                                                                                                                                                                                                                                                                                                                                                                                       1941 TCTTCTTTAAGAGGGCAATGGAAGGGCACACACTACTTATGTGCTGGAAGAATGACT 2000
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                                                                                                                                                                                                  01-JAN-1900
                                                                                                                                                                                                                         5260432-1 STANDARD;
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                                              Sequence
                                                                                                                                                                                                             XXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: lin
MOLECULE TYPE:
HYPOTHETICAL: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE PC-DOS/MS-DOS
COERRATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: KIT, Gordon
                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                FILING DATE: 22-JUN-1989
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                                              LENGTH: 1576
ence 1707 BP;
                                                                                                APPLICATION NUMBER:
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l similarity 63.7%;
123; Conservative
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 Conservative
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          3.0%;
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                                                                                                 US/07/370,407
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Pred. No.
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0; Mismatches
          Score 51; DB 3; I
Pred. No. 2.91e-20;
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 Mismatches
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                                                285 T; 131 other;
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                       Length 1576;
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Best Local S
Matches 12
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MOLECULE TYPE: genomic DNA
SEQUENCE 387 BP; 109 A; 92 C;
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Sequence 1, Application US/08087151
Patent No. 5468624
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APPLICANT: E. Brad Thompson
APPLICANT: Lynne V. Nazareth
TITLE OF INVENTION: ANTI-TUMOR ACTIVITY OF A MODIFIED FRAGMENT
TITLE OF INVENTION: OF THE GLUCOCORTICOID RECEPTOR
NUMBER OF SEQUENCES: 3
                                                188 TCTGCCTGGTGTGCTCTGATGAAGCTTCAGGATGTCATTATGGAGTCTTAACTTGTGGAA 247
                                                                                                                                                                                                                           TELEFAX: 512-474-7577
TELEX: No. 5468624 Applicable
INFORMATION FOR SEQ ID NO: 1:
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                                                                                 2.8%;
Local Similarity 63.0%;
nes 126; Conservation
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 512-320-7200
                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Hodgins, Daniel S.
REGISTRATION NUMBER: 31,0
                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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ZIP: 77210
GCTGTAAAGTTTTCCTTCAAAAGAGCAGTGGAAGGACAGCACAATTACCTATGTGCTGGAA
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                                   tctgcgctgtctgcagcgattacgcatcgggatatcactatggagtctggtcgtgtgaag 595
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REFERENCE/DOCKET NUMBER: UTSG:141/HOD
                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/087,151
FILING DATE: July 7, 1993
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Pred. No. 2.34e-17
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Best Local
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LENGTH: 387 base pairs
308 GGAATGATTGCATCATCGCGATAAAATT-CGAAAAAACTGCCCAGCATGCCGCTATCGAA 366
                        596 gatgtaaggccttttttaaaaagaagcattcaaggacataatgattatatttgtccagcta 655
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FILING DATE: July 7, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Hodgins, Daniel S.
REGISTRATION NUMBER: 31,026
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REFERENCE/DOCKET NUMBER: UT:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-320-7200
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CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, W
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TITLE OF INVENTION: ANTI-TUMOR ACTIVITY OF A MODIFIED FRAGMENT
TITLE OF INVENTION: OF THE GLUCOCORTICOID RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                             GCTGTAAAGTTTTCTTCAAAAGAGCAGTGGAAGGACAGCACAATTACCTATGTGCTGGAA 307
                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
                                                                         tctgcgctgtctgcagcgattacgcatcgggatatcactatggagtctggtcgtgtgaag 595
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TELEFAX: 512-474-7577
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                                                                                                                              126;
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Similarity 63.0%;
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Application
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Pred. No. 2.34e-17;
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APPLICANT: Sloan-Kettering
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                                                                                                                        SEQUENCE 2928 BP; 582 A; 1011 C; 789 G; 546 T; 0 OTHER
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           424
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                                            364 TGCTTTGTCTGTCAGGACAAGTCCTCAGGCTACCACTATGGGGTCAGCGCCTGTGAGGGC 423
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TELEX: (212) 422523 COO
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                   FILING DATE: 22-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 673,83
FILING DATE: 22-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WHITE, JOHN P
REGISTRATION NUMBER: 28,678
                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/023
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                             IMMEDIATE SOURCE:
CLONE: hRAR ALPHA
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                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                    TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                    TELEPHONE: (212) 977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: Pater+**
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                                                                                                                                  NAME/KEY: CDS
LOCATION: 103..14
OTHER INFORMATION:
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CLASSIFICATION:
           TGCAAGGGCTTCTTCCGCCGCAGCATCCAGAAGAACATGGTGTACACGTGTCACCGGGAC 483
                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: sing
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120; Conservative
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Pred. No. 8.39e-14
0; Mismatches 7
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AND TREATMENT O
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 5171671
                                                                                                                                                                                                                                                                                              SEQ ID NO:1:
                                                                                                                                                                                                                                                                   LENGTH: 2940
Sequence 3185 BP; 594 A; 1010 C; 790 G; 546 T; 245 other:
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718
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FILING DATE: 06-AUG-1990
PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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                                                                            AAGAACTGCATCATCAACAAGGTGACCCGGGAACCGCTGCCAGTACTGCCGACTGCAGAAG
                                                                                                                                 TGCAAGGGCTTCTTCCGCCGCAGCATCCAGAAGAACATGGTGTACACGTGTCACCGGGAC
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tgttacgaagtgggaatg
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                                                                                                        tgtaaggccttttttaaaagaagcattcaaggacataatgattatatttgtccagctaca
                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 276,536 FILING DATE: 30-NOV-1988
                                                                                                                                                                                                                 120;
                                                                                                                                                                                                                            2.5%;
Similarity 60.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD; DNA; UNC;
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0; Mismatches 78;
                                                                                                                                                                                                                                          Score 42;
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                                                                                                                                                                                                                                          DB 3;
                                                                                                                                                                                                                                           Length 2940
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Search completed: Tue Job time: 79 secs. NOV ω 04:58:08 1998

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_nn n.a. n.a. database search, using Smith-Waterman algorithm

Run on: Tue Nov 3 03:32:21 1998; MasPar time 2544.39 Seconds 1354.241 Million cell updates/sec

Tabular output not generated.

Title: >US-08-906-365-1 (1-1686) from US08906365.seq 1686

Description:
Perfect Score:
N.A. Sequence:
Comp: 1 cagccattatacttgcccac......agaacccacagtctcagtga 1686 gtcggtaatatgaacgggtg......tcttgggtgtcagagtcact

Scoring table: TABLE default Gap 6

Nmatch STD:

Searched: 552174 seqs, 1021863385 bases

× 2

Dbase 0; Query 0

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: emb155

Database:

1:em_ba 2:em_htg 3:em_hum1 4:em_hum2 5:em_in 6:em_om 7:em_or 8:em_ov 9:em_pat 10:em_pl 11:em_ro genbank107
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Statistics: Mean 11.383; Variance 4.965; scale 2.293

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	Ħ	Description	Pred. No.
—	1684	99.9	1740	21	AB006590	Homo sapiens mRNA for	0.00e+00
2	1683	99.8	2011	21	AF051427	sapiens	0.000+0
w	1496	22	2041	اد	3E051436		0 0
، ر	1490	88.	704T	17	AF-051428	Homo sapiens estrogen	0.00e+0
4	1496	88.7	2745	21	AF060555	Homo sapiens estrogen	0.00e+00
ر. د	1495	88.7	3593	21	AB006589	Homo sapiens mRNA for	0.00e+00
σ	1452	86.1	1460	စ	A61586	Sequence 4 from Patent	0.00e+00
7	1450	86.0	1560	20	HSRNAERB	H.sapiens mRNA for est	0.00e+00
8	1140	67.6	1650	22	RNAJ2602	Rattus norvegicus mRNA	0.00e+00
9	1136	67.4	2555	22	RNU57439	Rattus norvegicus estr	0.00e+0
10	1136	67.4	2568	ø	A61583	Sequence 1 from Patent	0.00e+00
11	1036	61.4	1621	22	AF042058	Rattus norvegicus estr	0.00e+0
12	1021	60.6	2152	22	MMU81451	Mus musculus estrogen	0.00e+0
13	1010	59.9	1458	9	A61588	Sequence 6 from Patent	0.00e+00
14	1010	59.9	1458	22	MMAJ220	Mus musculus mRNA for	0.00e+00
15	781	46.3	1215	<u>ي</u>	AF074599	Homo saniens estronen	0 000+00

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Rainbow trout estrogen Sparus aurata estrogen		H.sapiens mRNA for est	Mouse estrogen recepto	Homo sapiens estrogen	Homo sapiens estrogen	estrogen receptor [rat	Rat mRNA for estrogen	Rat mRNA for estrogen	Taeniopygia guttata es	Š	9	16	Sequence 1 from Patent	Human estrogen recepto	on P	Chicken mRNA for estro	O.aries mRNA for estro	Chrysophrys major mRNA	S.scrofa mRNA for estr	Oryzias sp. mRNA for e	Homo sapiens estrogen	C. jacchus mRNA for est	0	norvegicus			Rattus norvegicus estr	varion not seatons mixing
.06e-	.17e-	.62e-	.04e-	. 89	.89e-	4e-13		2.54e-137		1.59e-149	1.59e-149	1.59e-149	1.59e-149				2.73e-153		3.57e-155			1.76e-225	3.93e-282		0.00e+00	0.00e+00	0.00e+00	0.000

ALIGNMENTS

RESULT 1	
LOCUS	
DEFINITION	iens mRNA
ACCESSION	
NID	g2911151
KEYWORDS	estrogen receptor beta.
SOURCE	Homo sapiens cDNA to mRNA.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
	Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (sites)
AUTHORS	Ogawa, S., Inoue, S., Watanabe, T., Hiroi, H., Orimo, A., Hosoi, T.,
	Ouchi, Y. and Muramatsu, M.
TITLE	The complete primary structure of human estrogen receptor beta (hER
	beta) and its heterodimerization with ER alpha in vivo and in vitro
JOURNAL	Biochem. Biophys. Res. Commun. 243 (1), 122-126 (1998)
MEDLINE	98139878
REFERENCE	2 (bases 1 to 1740)
AUTHORS	Ogawa, S.
TITLE	Direct Submission
JOURNAL	Submitted (13-AUG-1997) to the DDBJ/EMBL/GenBank databases. Sumito
	hemist
	Morohongo, Moroyama, Iruma-gun, Saitama 350-04, Japan
	(E-mail:suogawa@saitama-med.ac.jp, Tel:81-492-76-1490, Fay:81-492-94-9751)
FEATURES	Location/Qualifiers
source	11/40
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CDS	991691
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	/db_xref="PID:g2911152"
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	YGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCYEVGMVKCG
	SRRERCGYRLVRRQRSADEQLHCAGKAKRSGGHAPRVRELLLDALSPEQLVLTLLEAE

BASE COUNT ORIGIN Query Match Best Local S Matches 168 661 601 606 541 546 481 486 421 426 361 366 301 306 241 246 181 186 121 126 846 721 726 999 781 786 61 66 σ GGTCGGCAGACCACAAGCCCAAATGTGTTGTGGCCAACACCTGGGCACCTTTCTCCTTTA CTTAATTCTCCTTCCTACAACTGCAGTCAATCCATCTTACCCCTGGAGCACGGCTCC TGCAAGGTGTTTTCTCAGCTGTTATCTCAAGACATGGATATAAAAAACTCACCATCTAGC GGGAACCGTTGCGCCAGCCCTGTTACTGGTCCAGGTTCAAAGAGAGGGATGCTCACTTCTGC atatacataccttcctcctatgtagacagccaccatgaatatccagccatgacattctat ATATACATACCTTCCTCCTATGTAGACAGCCACCATGAATATCCAGCCATGACATTCTAT cttaattctccttcctacaactgcagtcaatccatcttacccctggagcacggctcc tgcaaggtgttttctcagctgctatctcaagacatggatataaaaaactcaccatctagc AAGGCCTTTTTAAAAGAAGCATTCAAGGACATAATGATTATATTTTGTCCAGCTACAAAT GCTGTCTGCAGCGATTACGCATCGGGATATCACTATGGAGTCTGGTCGTGTGAAGGATGT gggaaccgttgcgccagccctgttactggtccaggttcaaagagggatgctcacttctgc AGCCCTGCTGTGATGAATTACAGCATTCCCAGCAATGTCACTAACTTGGAAGGTGGGCCT GGCCACGCGCCCCGAGTGCGGGAGCTGCTGCTGGACGCCCTGAGCCCCGAGCAGCTAGTG cagtgtacaatcgataaaaaccggcgcaagagctgccaggcctgccgacttcggaagtgt CAGTGTACAATCGATAAAAACCGGCGCAAGAGCTGCCAGGCCTGCCGACTTCGGAAGTGT aaggccttttttaaaagaagcattcaaggacataatgattatatttgtccagctacaaat gctgtctgcagcgattacgcatcgggatatcactatggagtctggtcgtgtgaaggatgt ggccacgcgccccgagtgcgggagctgctgctggacgccctgagccccgagcagctagtg 99.9%; hl Similarity 99.9%; 1685; Conservative 425 Ø PPHYLISRPSAPFTEASMMMSLTKLADKELVHMISWAKKIPGFVELSLFDQVRLLESC MMEVLMMSLMKSIDHPGKLIFAPDLVLLDRDEGKOVEGILEIFDMLLATTSRFFELKL OHKEYLCVKAMILLMSSMYPLVTATQDADSSRKLAHLLNAVTDALVWVIAKSGISSQQ QSMRLANLMLLSHVRHASNKGMEHLLNMKCKNVVPVYDLLLEMLNAHVLRGCKSSIT GSECSPAEDSKSKEGSQNPQSQ"

3 463 c 459 g 393 t Score Pred. 0; M re 1684; DB 21; d. No. 0.00e+00; Mismatches 1; Length Indels 1740; 0 Gaps 125 60 65 485 420 425 305 245 180 185 120 360 365 300 600 605 545 480 900 840 845 780 785 720 725 660 665 540 0;

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CTCACCCTCCTGGAGGCTGAGCCGCCCCATGTGCTGATCAGCCGCCCCAGTGCGCCCTTC

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KEYWORDS SOURCE ORGANISM

Homo

sapiens

hordata; Vertebrata; Hominidae; Homo.

Mammalia;

Eutheria;

REFERENCE AUTHORS

Eukaryota; Metazoa; Chordata; V. Primates; Catarrhini; Hominidae, 1 (bases 1 to 2011)

Moore, J. T., McKee, D. D., Moore, L. Slentz-Kesler, K., Horne, E. L., K. Willson, T. M.
Cloning, Ligand Binding and Func Receptor beta isoforms
Unpublished

Functional

Activity

Human

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Moore, J.T., McKee, J.Slentz-Kesler, K., J. Willson, T.M.
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Submitted (25-FEB-1998)
Drive, RTP, NC 27709, Ut
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Submitted (25-FEB-1998) Molecular
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Moore, J.T., McKee, D.D., M
Horne, E.L., Kliewer, S.A.,
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/db_xref="pID:g2961559"
/db_xref="pID:g2961559"
/translation="MDIKNSPSSLNSPSSYNCSQSILPLEHGSIYIPSSYVDSHHEYP
AMTFYSDAVMNYSIPSNYTNLEGGFGRQTTSPNVLWPTPGHLSPLYVHRQLSHLYAEP
QKSPWCEARSLEHTLPYNRETLKRKVSQNRCASPYTGPGSKRDAHFCAVCSDYASCYH
YGVWSCEGCKAFFKKSIQGHNDYICPATNQCTIDKNRKKSQQACRLRKCYEVGMYKCG
SRRERCGYRLVVRORSADEQLHCAGKAKRSGGHAPRVRELLLDALSPEQLYLTLLEAE
PPHVLISRPSAPFTEASMMMSLTKLADKELVHMISWAKKIPGFVELSLFDQVRLLESC
WMEVLMWGLMWRSIDHFGKLIFAPDLVLDRDEKCVEGILEIFDMLLATTSRFRELKL
QHKEYLCVKAMILLUSSMYPLYDATQDADSSRKLAHLLNAVTDALYWVIAKSGISSQQ
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1 (bases 1 to 2745)
Moore, J.T., McKee, D.D., Slentz-Kesler, K., Moore, Su, J.L., Horne, E.L., Kliewer, S.A., Lehmann, J.M., Direct Submission
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//db_xref="pit:g3091286"
//tabslation="MolKN9PSSLNSPSSYNCSQSILPLEHGSIYIPSSYVDSHHEYP
//tabslation="MolKN9PSSLNSPSSYNCSQSILPLEHGSIYIPSSYVDSHHEYP
AMTFYSPAVNNYSIPSNVTNLEGGPGROTTSPNVTWPTPGHLSPLYVHRQLSHLYAEP
QKSFWCEARSLEHTLEVNRETLKRKVSGNRCASPVTGPGSKDAHFCAVCSDYASGYH
YGYWSCEGCKAFFKRSIGGHNDYICPATNQCTIDKNRRKSQOACRLRKCYEVGMYKCG
SRRERCGYRLVRQRSADEQLHCAGKAKRSGGHAPRVRELLLDALSPEQLVLTLLEAE
PHYLISRPSAPFTEASMMMSLTKLADKELYHMISWAKKIPGYBLLEHDQVRLLESC
WHEVLMMGLWARSIDHPKLIFAFDLYLDRDEGKCVEGILEIFDMLLATTSRFRELKL
QHKEYLCVKAMILLNSMYPLVTATQDADSSRKLAHLLNAVTDALYWVIAKGGISSQQ
QSMRLANLLMLLSHYRHASSLSLSWRLFMLREASCHGVRQTPGGAHMSVSRSRSFEAC
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                                                                        TGTACCCTCTGGTCACAGCGACCCCAGGATGCTGACAGCAGCCGGAAGCTGGCTCACTTGC
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 CTTAATTCTCCTTCCTACAACTGCAGTCAATCCATCTTACCCCTGGAGCACGGCTCC
                                        AGCCCTGCTGATGAATTACAGCATTCCCAGCAATGTCACTAACTTGGAAGGTGGGCCT 1482
                                                                                          ATATACATACCTTCCTATGTAGACAGCCACCATGAATATCCAGCCATGACATTCTAT 1422
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1497; Conser
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Molecular cloning and characterization of human estrogen receptor beta cx: a potential inhibitor of estrogen action in human Nucleic Acids Res. 26, 3505-3512 (1998)

2 (bases 1 to 3593)
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QKSPMCEARSLEHTLFVNRETLKRKVSGNCCASPVTGPGSKRDAHFCAVCSDYAKGYH
YGVMSCEGCKAFFKRS JOGHNDY I CFATNOCT I DKNRRKSCOACRLRKCYEVGMYCG
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WMEVLLMGLWRRSI DHPGKLIFAPDLVLDRDEGKCVEGILEI FDMLLATTSRFRELKL
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1276. .2763
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	מט	1483	GGTCGGCAGACCACAAGCCCCAAATGTGTGTGGCCAACACCTGGGCACCTTTCTCCTTTA 1542
	Qy	301	ggtcggcagaccacaagcccaaatgtgttgtggccaacacctgggcacctttctccttta 360
	Дb		GTGGTCCATCGCCAGTTATCACATCTGTATGCGGAACCTCAAAAGAGTCCCTGGTGTGAA 1602
	Qy		tggtccatcgccagttatcacatctgtatgcggaacctcaaaagagtccctggtgtgaa 42
	당 당	1603	GCAAGATCGCTAGAACACACCTTACCTGTAAACAGAGAGACACTGAAAAGGAAGG
	Db	1663	GTTGGGCAGCCCTGTTACTGGTCCAGGTTCAAAGAGGGATGCTCACTTCTGC 17
	Qy	481	gggaaccgttgcgccagccctgttactggtccaggttcaaagagggatgctcacttctgc 540
	Дb	1723	IGCAGCGATTACGCATCGGGATATCACTATGGAGTCTGGTCGTC
	Qy	541	gctgtctgcagcgattacgcatcgggatatcactatggagtctggtcgtgtgaaggatgt 600
	Дb	1783	TTTTAAAAGAAGCATTCAAGGACATAATGATTATATTTTGTCCAGG
	Qy	601	aaggccttttttaaaagaagcattcaaggacataatgattatattttgtccagctacaaat 660
	Db	1843	CAGTGTACAATCGATAAAAACCGGCGCAAGAGCTGCCCAGGCCTGCCGACTTCGGAAGTGT 1902
	Qy	661	agtgtacaatcgataaaaaccggcgcaagagctgccaggcctgccgacttcggaagtg
	Db	1903	TACGAAGTGGGAATGGTGAAGTGTGGCTCCCCGGAGAGAGA
	Qy	721	acgaagtgggaatggtgaagtgtggctcccggagagagag
	Дδ	1963	CGGAGACAGAGAAGTGCCGACGAGCAGCTGCACTGTGCCGGCAAGGCCAAGAGAAGTGGC 2022
	Qy	781	ggagacagagaagtgccgacgagcagctgcactgtgccggcaaggccaagagaagtgg
_,	Db	2023	GGCCACGCGCCCCGAGTGCCGGAGCTGCTGCTGGACGCCCTGAGCCCCGAGCAGCTAGTG 2082
	Qγ	841	gccacgcgccccgagtgcgggagctgctgctggacgccctgagccccgagcagctagt
	d d	2083	CTCACCCTCCTGGAGGCTGAGCCGCCCCATGTGCTGATCAGCCGCCCCAGTGCGCCCCTTC 2142
	롸 .	2143	COGAGGCCTCCATGATGATGTCCCTGACCAAGTTGGCCGACAAGGAGTTGGTACACATG 22
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	Db	ö	TCAGCTGGGCCAAGAAGATTCCCCGGCTTTGTGGAGCTCAGCCTGTTCGACCAAG
	Qy	1021	gcg
	DЪ	2263	CTCTTGGAGAGCTGTTGGATGGAGGTGTTAATGATGGGGCTGATGTGGCGCTCAATTGAC 2322
	Qy	1081	tettggagagetgttggatggaggtgttaatgatggggetgatgtggegeteaattg
	Db	2323	CACCCCGGCAAGCTCATCTTTGCTCCAGATCTTGTTCTGGACAGGGATGAGGGGAAATGC 2382
	Qy	1141	cccggcaagctcatctttgctccagatcttgttctggacagggatgagggaaatg
	рb	2383	-≱
	Qy	1201	tagaaggaattotggaaatotttgacatgotootggcaactacttcaaggtttcgac
	DЪ	2443	TTAAAACTCCAACACAAAGAATATCTCTGTGTGTCAAGGCCATGATCCTGCTCAATTCCAGT 2502
	Qy	N	aaaactccaacacaaagaatatctctgtgtcaaggccatgatcctgctcaattccagt 132
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                     CCAGCTACAAATCAGTGTACAATCGATAAAAACCGGCGCAAGAGCTGCCAGGCCTGCCGA
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                                   ccagctacaaatcagtgtacaatcgataaaaaccggcgcaagagctgccaggcctgccga
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SOURCE KEYWORDS ORGANISM

human.

receptor

H.sapiens X99101 estrogen g1518262

HSRNAERB

Homo sapiens Eukaryotae; Vertebrata;

mitochondrial Eutheria; Prin

rial eukaryotes; Metazoa; Primates; Catarrhini; Ho

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RESULT 8
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18-APR-1998 (clone

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Group, ZENECA Central Toxicology
Macclesfield, Cheshire SK10 4TJ,
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Submitted (17-APR-1997) Aldridge T.C., Molecular Endoc Submitted (17-APR-1997) Aldridge T.C., Molecular Endoc Group, ZENECA Central Toxicology Laboratory, Alderley Macclesfield, Cheshire SK10 4TJ, ENGLANG
3 (bases 1 to 1650)
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Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 1650)
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/product="estrogen receptor beta"
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Patent number WO9709348-A/1,
KAROBIO AB (SE).
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ae; Murinae; Rattus.
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                                                                                                                                                 Submitted (09-JAN-1998) Research, Eastern Point
                                                                                                                                                                                               Endocrinology (1998) In 2 (bases 1 to 1621)
                                                                                                                                                                                                                      Identification of estrogen receptor estrogen receptor beta expressed in
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                                                                                                                                  (09-JAN-1998) Molecular
Eastern Point Road, Grot
Location/Qualifiers
 /codon_start=1
/product="estrogen
                         /note="steroid hormone receptor"
                                   /gene="ERbeta"
                                                            /gene="ERbeta"
                                                                                    /db_xref="taxon:10116"
                                                                                                  /strain="Sprague-Dawley"
                                                                                                            organism="Rattus norvegicus"
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ciurognathi; Muridae; Murinae; l
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                                          AAGAGAAACGGTGGGCATGCACCCCGGGTGAAGGAGCTACTGCTGAGCACCTTGAGTCCA
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aagagaagtggcggccacgcgccccgagtgcgggagctgctgctggacgccctgagcccc
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/note="encodes |
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LSLLDQVRLLESCMMEYLMVGLMWRSIDHPGKLIFAPDDVLDEDEGKCVEGILEIFDM
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VMVIAKSGISSQQSSVLANLLMLLSHVRHISNKGMEHLLSMKCKNVVPVYDLLLEML
NAHTLRGYKSSISGSECSSTEDSKNKESSQNLQSQ"
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lrkcyevgmvkcgsrrercgyrivrrqrssseqvhclskakrngghaprvkelllstl
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Tremblay,G.B., Tremblay,A., Copeland,N. Jenkins,N.A., Labrie,F. and Giguere,V. Cloning, chromosomal localization, and murine estrogen receptor beta Mol. Endocrinol. 11 (3), 353-365 (1997)
                                                                              Mus.
                                                                                                                                                          g1912467
nuclear receptor;
                                                                                                                                                                                 Mus musculus
U81451
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Vertebrata;
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(Estrb)
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                                                     Gilbert, D.
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                                                                                           Muridae;
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ACTTCGCAAGTGTTACGAAGTAGGAATGGTCAAGTGTGGATCCAGGAGAGAAAGGTGTGG
                                                       tccagctacaaatcagtgtacaatcgataaaaaccggcgcaagagctgccaggcctgccg
                                                                             TCCAGCCACGAATCAGTGTACCATAGACAAGAACCGGCGTAAAAAGCTGCCAGGCCTGCCG
                                                                                                                                  TGCTCACTTCTGCGCCGTCTGCAGTGATTATGCATCTGGGTATCATTACGGTGTCTGGTC
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Direct Submission
Submitted (09-DEC-1996) Molecular
Hospital, 687 Pine Avenue West, MC
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//db_xref="plD:g1912468"
//db_xref="plD:g1912468"
//translation="MIFYSPAVMNYSVPSSTGNLEGGPVRQTASPNVLWPTSGHLSPL
ATHCQSSLLYAEPQKSPWCEARSLEHTLPVNRETLKRKLGGSGCASPVTSPSAKRDAH
FCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACR
LRKCYEVGMVKCGSRRERCGYRLVRRQNSASEOVHCLNKAKRTSGHTPRVKELLLNSL
SPBQLVTLLLEAEPAVVLVSRSSMPFTEASMMYSLTKLADKELYMIGWAKKIFGFVE
LSLLDQVRLLESCWMEVLMVGLMWRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFGM
LLATTARFRELKLQHKEYLCVEAMILLNSSMYPLATASQEAESSRKLTHLLNAVTDAL
VWVISKSGISSQQQSVRLANLLMLLSHVRHISNKGMEHLLSMKCKNVVPVYDLLLEML
NAHTLRGYKSSISGSECCSTEDSKSKESQNLQSQ"
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                                                                                                                Pettersson, K., Grandien, K., Kuiper, G.G. and Gustafsson, The mouse estrogen receptor beta form estrogen response binding heterodimers with the estrogen receptor alpha
                                                    Submitted (15-JUL-1997)
Nutrition, Karolinska I
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estrogen receptor;
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//db_xref="piD:el192418"
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//db_xref="piD:el192418"
//db_xref="piD:el2370297"
//db_xref="piD:g2370297"
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FCAVCSDYASGYHYGYWSCEGCKAFFKRSIGCHNDYICPATNOCTIDKNRRKNCOACR
LRKCYEVGMVKCGSRRERCGYRIVRRORASAEQVHCLINKAKRTSGHTPRVKELLINSL
SPEQLVLTLLEAEPPNVLVSRSHSTTSASMMSLTKLADKELVHMIGWAKKIPGFVE
LSLLDQVRLLESCWMEVLMVGLMWRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFDM
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Homo sapiens
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                                    Brandenberger, A.W., Lebovic, D., Taylo
Direct Submission
Submitted (25-JUN-1998) Reproductive
University of California, San Francis
Francisco, CA 94143-0556, USA
                                                                                                         Eukaryota; Metazoa; Chordata; Vertebrata; Mammal primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1215) Brandenberger, A.W., Lebovic, D., Taylor, R.N. and Homo sapiens estrogen receptor beta 5/6 splice v
                                                                                               Unpublished
                                                                                                                                                            Homo sapiens
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                     TGACCAAGTTGGCCGACAAGGAGTTGGTACACATGATCAGCTGGGCCAAGAAGATTCCCG
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tgaccaagttggccgacaaggagttggtacacatgatcagctgggccaagaagattcccg
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/db_xref="ptD:9389023"
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/translation="psWrvINLEGGPGRQTTSDNVLWPTPGHLSPLVVHRQLSHLYAEP
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/GKSPWCEARSLEHTLPVNRETLKRKVSGNRCASPVTGPGSKRDAHFCAVCSDXASGYH
/GVWSCEGCKAFFKRSIQGHNDYICPARNQCTLDKNREKSCQACHLKKCYEVCWYKCG
SREERGGYRLVBRORSADEQLHCAGKAKRSGHAPFWRELLLDALSPEDLVLTILLAE
SREERGGYRLVBRORSADEQLHCAGKAKRSGHAPFWRELLLDALSPEDLVLTILDADSSRK
LAHLLNAVTDALVWVIAKSGISSQQGSKFLANLLMLLSHVRHASKGKEHLLNNKCKN
VVPVYDLLLBRINGHVLAGKSSITGSECSPAEDSKSKEGSQNPQSQ"
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Db 781 G 781
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Search completed: Tue Nov 3 04:15:08 1998
Job time: 2567 secs.

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MPsrch_nn n.a. n.a. database search, using Smith-Waterman algorithm

Run on: Tue Nov 3 04:51:42 1998; MasPar time 278.07 Seconds 824.913 Million cell updates/sec

Tabular output not generated.

Title: >US-08-906-365-1 (1-1686) from US08906365.seq

1686

Description:
Perfect Score:
N.A. Sequence:
Comp: 1 cagccattatacttgcccac......agaacccacagtctcagtga 1686 gtcggtaatatgaacgggtg......tcttgggtgtcagagtcact

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Scoring table: TABLE Gap 6 default

Nmatch STD: Dbase 0; Query 0

Searched: 188442 seqs, 68026449 bases × N

Post-processing:

Minimum Match 0% Listing first 45 summaries

Database:

n-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part20 31:part31 32:part32 33:part13
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40

Statistics: Mean 9.451; Variance 5.146; scale 1.837

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Query Match Length	DB	ij	Description	Pred. No.
1	1667	98.9	1936	38	T88415	Human oestrogen recep	0.00e+00
N	1452	86.1	1460	29	T62843	oestrogen	0.00e+00
ω	1434	85.1	1434	37	T88412	oestrogen	0.00e+00
4	1247	74.0	1251	37	T88413	oestrogen	0.00e+00
U	1247	74.0	1257	38	T88414	oestrogen	0.00e+00
o	1136	67.4	2568	29	T62842	Rat oestrogen recepto	0.00e+00
7	1010	59.9	1458	29	T62844	Mouse oestrogen recep	0.00e+00
œ	197	11.7	4963	17	T06873	PhCMV*-1 promoter and	3.54e-124
vo	197	11.7	4963	<u>1</u> 3	Q76270	PhCMV*-1-controlled p	3.54e-124
10	195	11.6	2092	N	N70880	cDNA encoding human o	1.18e-122
11	127	7.5	204	15	Q85976	Human estrogen recept	1.90e-71
c 12	71	4.2	3460	25	T42193	Fragment of pig oestr	6.97e-31
13	68	4.0	2153	N	N80922	Sequence encoding hum	8.56e-29

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13-MAR-1997.
09-SEP-1996; GB-018.
15-MAR-1996; GB-005.
11-APR-1996; GB-007.
08-MAY-1996; GB-007.
08-MAY-1996; GB-009.
(KARO-) KARO BIO AB EDMARK E. Gustafss.
WPI; 97-192842/17.
P-PSDB; W14724.
New isolated oestro
                                                                                 treating disease
                                                                                                                                                                                                                                                                                                        orphan receptor; oestrogen receptor beta (ER-beta) cDNA.
Orphan receptor; oestrogen receptor beta; ER-
nuclear receptor; prostate cancer; benign pro
ovary cancer; cardiovascular 4000000
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Claim 6; Fig 13B; 45pp; English.

A CDNA clone (762843) codes for a novel human oestrogen recepto: A cDNA clone (762843) codes for a lesignated ER-beta. It was isolated from a human testis cDNA library using rat ER-beta cDN (see also T62842) as probe. The human ER-beta gene was mapped to chromosome 14 region 14922-23. Rat, human and mouse ER-beta (W14723-25) can be used to isolate molecules for use in the
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995; GB-015272.
996; GB-005550.
996; GB-007532.
996; GB-009576.
KARO BIO AB.
Gustafsson J.
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Query Match
Best Local Similarity
Matches 1455; Conser
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diseases, osteoporosis, prostate or ovarian cancer or ben-
prostatic hyperplasia and to test environmental chemicals
oestrogenic activity.
Sequence 1460 BP; 352 A; 379 C; 411 G; 318 7
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1. No. 0.00e+00;
Mismatches 3;
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Query Match
Best Local Simil
Matches 1434;
                                                                                    Homo sapiens.
EP-798378-A2.
01-OCT-1997.
25-MAR-1997; 200903.
25-MAR-1996; EP-203284.
26-MAR-1996; EP-200820.
(ALKU ) AKZO NOBEL NV.
Dijkema R, Mosselman S;
WPI; 97-473188/44.
P-PSDB; W33212.
DNA encoding estrogen recidentify novel ligands of Claim 5; page 13-14; 45pg
                               DNA encoding estrogen receptor - useful in screening assay to identify novel ligands or hormonal analogues Claim 5; Page 13-14; 45pp; English.

This sequence encodes a novel osstrogen binding protein. The cDNA sequence which encodes this protein can be alternatively spliced resulting in the detection of additional transcripts (see T88413). This receptor is able to bind and be activated by estradiol, estone estriol, can be used in a screening assay for the identification of drugs e.g. novel ligands or hormonal analogues.

Sequence 1434 BP; 347 A; 373 C; 406 G; 308 T;
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estone; es
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estrogen receptor protein
en receptor protein; sterc
estriol; screening; ds.
85.1%;
llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                              cDNA;
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Score Pred.
re 1434; DB 37;
1. No. 0.00e+00;
Mismatches 0;
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oid; alternative
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Indels
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                                                                                                                                                                           DNA encoding estrogen receptor - useful in screening assay to identify novel ligands or hormonal analogues

PS Claim 5; Page 14-15; 45pp; English.

CC This partial sequence encodes a splice variant of a novel oestrogen binding protein, detected by screening a human testis cDNA library.

CC binding protein, detected by screening a human testis cDNA library.

CC this protein contains an alternative exon 8 (exon 8B) of the novel contains an alternative exon 8 (exon 8B) of the novel contains an alternative splicing reaction, the reading frame encoding the novel receptor is immediately terminated, creating a truncation of the carboxy terminus of the novel receptor.

CC This novel receptor is able to bind and be activated by estradiol, estone and estriol, and can be used in a screening assay for the identification of new drugs e.g. novel ligands or hormonal analogues, however this contain the contain an AF-2 region and therefore probably lacks the ability to modulate transcription of target genes in a ligand dependent
                                        Query Ma
Best Loc
Matches
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estone; estricl; scr
Homo sapiens
EP-798378-A2.
01-0CT-1997, 200903.
25-MAR-1996; EP-2033
22-NOV-1996; EP-2033
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                                        Local Simi hes 1247;
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96; EP-203284.
96; EP-200820.
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MOSSElman S;
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larity 100.0%;
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Homo sapiens.
EP-798378-A2.
01-OCT-1997; 200903.
25-MAR-1997; 200903.
22-NOV-1996; EP-2003284
26-MAR-1996; EP-200820
(ALKU ) AKZO NOBEL NV.
Dijkema R, Mosselman S
WPI; 97-473188/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding estrogen receptor - useful in screening assay to identify novel ligands or hormonal analogues Claim 5; Page 28-29; 45pp; English.

This sequence encodes splice variant of a novel cestrogen binding protein isolated from human thymus tissue. This protein contain an alternative exon 8 (exon 8C) of the novel cestrogen receptor represented in T88412.

This novel receptor is able to bind and be activated by estradiol, estone and estriol, can be used in a screening assay for the identification of new drugs e.g. novel ligands or hormonal analogues. This variant does not contain an AF-2 region and therefore probably lacks the ability to modulate transcription of target genes in a ligand dependent fashion.

Sequence 1257 BP; 297 A; 327 C; 355 G; 278 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB;
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Local Similarity 100.0%;
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Mosselman S;
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Pred. No. 0.00e+00;
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08-SEP-1995; GB-018272.

15-MAR-1996; GB-005550.

11-APR-1996; GB-007532.

08-MAY-1996; GB-009576.

(KARCO-) KARO BIO AB.

Enmark E., Gustafsson J,

WPI; 97-192842/17.

WPI; 97-192842/17.
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T62842 standard; cDNA; 2568 br.
T62842;
08-JUN-1997 (first entry)
Rat oestrogen receptor beta (ER-beta) cDNA.
Rat oestrogen receptor beta; F
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Orphan receptor; oestrogen receptor beta; ER-beta;
nuclear receptor; prostate cancer; benign prostatic
ovary cancer; cardiovascular disease; osteoporosis;
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13-MAR-1997.
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A cDNA clone (76.842) codes for a novel rat oestrogen receptor. A set of related nuclear receptor (W13723), designated ER-beta. A set of degenerate primers based on conserved sequences of the DNA-binding domain and ligand binding domain of nuclear receptors were used to amplify rat prostate cDNA. The PCR prod. was used to screen a rat prostate cDNA library to obtain the ER-beta cDNA. This was then used to obtain human ER-beta cDNA (see also 76.8843) from a human testis cDNA library. Rat, human and mouse ER-beta (W14723-25) can be used to isolate molecules for use in the treatment of cardiovascular diseases, central nervous system of diseases, osteoporosis, prostate or ovarian cancer or benign prostatic hyperplasia and to test environmental chemicals for coestrogenic activity.
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A cDNA clone (T62844) codes for a novel mouse oestrogen receptor-
related nuclear receptor (W13725), designated ER-beta. Rat, human
and mouse ER-beta (W14723-25) can be used to isolate molecules for
use in the treatment of cardiovascular diseases, central nervous
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                                                      Q76270 standard; DNA; 4963 BP.
Q76270;
Q76270:
17-JUL-1995 (first entry)
PhCMV*-1-controlled progesterone receptor
tTA; transactivator; tetracycline-controllable transactivator;
conditional inactivation; homologous recombination; gene expre
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progesterone receptor; Human cytomegalovirus W09429442-A.

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larity 66.7%;
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14-JUN-1993;
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The minimal promoter PhCMV*-1 is based on the human CMV intermediate-early promoter (with enhancer region remover to a tetracycline operator, teto. The promoter is used express tTA transactivator in host cells. In clone pUHD (given in 076269), CDNA for rabbit progesterone receptor the control of PhCMV*-1.
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WPI; 95-036472/05.
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Disclosure; Fig. 1-1 - 1-2; 26pp; English.

The cDNA can be used in an expression system to express human oestrogen receptor protein. The coding sequence is operably linked control sequences compatible with eukaryotic host cells. This metho allows expression under conditions which favour appropriate post-translational processing. It produces large amts. of purified prote useful in the design of agonist and antagonist cpds., for the study the mechanism of action of the steroid binding proteins in general, and for use in diagnostic assays for the proteins or antibodies to them. These assays are important in, eg the diagnosis of tumour sensitivities to steroid metabolism. Suitable host cells are VERO, HeLa and CHO cells.
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                                                       tecteccageageaatecatgegeetggetaaceteetgatgeteetgteecaegteagg
                                                                                                              tcacttg--ctgaacgccgtgaccgatgctttggtttgggtgattgccaagagcggcatc
                                                                                                                                                                     tccagtatgtaccctctggtcacagcgacccaggatgctgac-agcagccggaagctggc
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larity 66.5%;
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Matches 16
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03-FEB-1995.
20-JUL-1993; 200333.
20-JUL-1993; JP-200333.
(MITU ) MITSUBISHI KASEI
WPI; 95-110650/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This cDNA encodes an estrogen receptor (a member of a receptor superfamily). It is disclosed in the patent specification. The invention concerns an EAR-1r gene (human erb-A related gene) encoding a nuclear receptor protein (R71565) derived from human osteosarcoma (HOS) cells. The expression of EAR-1r is most abundant in the brain and was detected slightly in heart and placenta. The receptor protein may be used for the investigation of generation, differentiation and growth of fat soluble physiological substances. Sequence 204 BP; 59 A; 46 C; 55 G; 44 T;
                                                   exon
                                                                                                                                                                                                            Pragment of pig oestrogen receptor gene. Pig; oestrogen receptor; exon; polymorphism; restriction fragment length polymorphism; Chiamplification; polymerase chain reaction; ds.
                                                                                                                                                                                                                                                                                     20-JAN-1997
Fragment of
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T42193 standard;
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Nuclear receptor protein
encoded by the EAR-1r g
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Disclosure; Page 6; 8pp; Japanese.
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Similarity 81.3%;
165; Conservative
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                                              /note= "undetermined length
between these nucleotides"
534..600
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human; erb-A related ge
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Pred. No. 1.
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1.90e-71;
~as 38;
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gene; estrogen recept
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ds.
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                                                                                         gap missing
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inese; American; PCR;
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primer;
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PI Tuggle CK, Vaske DA;

DR WPI; 96-401592/40.

PT Screening pigs for high litter size - by identifying a polymorphism

PT in the pig oestrogen receptor gene in a DNA sample

Screening pigs for high litter size - by identifying a polymorphism

PT in the pig oestrogen receptor gene in a DNA sample

CC This is a fragment of the pig oestrogen receptor (ESR) gene including

CC This is a fragment of the pig oestrogen receptor (ESR) gene including

CC exon 3. The sequence covers the region contg. a polymorphic PvuII

CC restriction enzyme site which is used as site for determining the ESR

CC allele carried by the animal. Restriction fragment length polymorphism

CC allele carried by the increased pig litter size dependent on the company of the pigs of this region revealed two alleles of 4.3 and 3.7 kb.

CC Both alleles are involved with increased pig litter size dependent on the company of the pigs born in each litter and company of the pigs born in each litter and company of the pigs born alive than pigs with the 4.3 kb allele. The allele can also be determined by PCR using the primers (T42194-T42201).
                                                                                                                               Query Match
Best Local
                                                                                                        Matches
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27-AUG-1996.
19-APR-1991; 687708.
19-APR-1991; US-687708.
19-ACT-1992; US-961819.
26-SEP-1994; US-961819.
26-SEP-1994; US-961819.
(BIOT-) BIOTECHNOLOGY RES & DI (LOWA) UNIV IOWA STATE RES EVENTS OF THE PROPERTY OF THE PROPERT
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95; Conser
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2011..2031
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2982..3002
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2729..2755
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2688..2693
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23-0CT-1987; U02782.
4-0CT-1986; US-922585.
20-0CT-1987; US-108471.
(SALK) Salk Inst for Biol S
Evans RM, Weinberger CA, Ho
WPI; 88-133242/19.
                                                                                                                                                                                       PhCMV*-1-controlled progesterone receptor
tTA; transactivator; tetracycline-controllable transactivator;
conditional inactivation; homologous recombination; gene expression;
gene regulation; gene therapy; tetracycline-resistance; tetR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor antagonist activity. They can also be used in diagnostic assays. Also claimed is pure DNA encoding oestrogen-related receptors hERR1 and hERR2 and hERR2. The new hERR1 and hERR2 receptors will provide the basis for development of an assay system that will lead to the identification of novel hormones.

Sequence 2153 BP; 445 A; 627 C; 624 G; 457 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 16; Fig V-2(B)-1 and -2; 243pp; English.

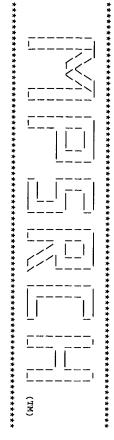
DNAs encoding hormone receptors and the hormone receptors themselves and the hormone receptor proteins and functional modified forms in quantities not previously possible. The receptor proteins can be used to screen cpds, for receptor agonist or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant DNA encoding hormone recpe comprising glucocorticoid, mineralocor and novel hormone receptors claim 16; Fig V-2(B)-1 and -2; 243pp;
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N80922 standard; cDNA; 2153
N80922;
                                                                                                                                                                       gene regulation; gene therap
transgenic animal; PhCMV*-1;
                                                                                                                          progesterone receptor;
Human cytomegalovirus '
                                                                                                                                                                                                                                                                                                                                                         Q76269 standard;
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133; Conser
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67.2%;
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Best Local S
Matches 12
                                                                                                                                                                                                                                         promoter linked to tet operon, and vectors and cells where gen expression is regulated by tetracycline Disclosure; Fig 9A-C; 37pp; English.

CDNA coding for the rabbit progesterone receptor was placed un control of the PhCMV*-1 promoter (see T06869), resulting in tetracycline-regulated expression vector pUHDpgr-3 contg. the sequence given in T06872. The construct was transfected into eukaryotic cells expressing the tTA transactivator (T06867) to allow tetracycline-regulated expression of the receptor.

Sequence 6244 BP; 1483 A; 1750 C; 1609 G; 1402 T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US5464758-A.
07-NOV-1995.
14-JUN-1993;
14-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T06872;
2365 tctgtggggatgaagcatcaggctgtcattatggtgtcctcacctgtgggagctgtaagg 2424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PhCMV*-1 promoter and rabbit progesterone receptor.
Transactivator; tTA; tet operator; tet0; gene expression;
tetracycline-responsive promoter; PhCMV*-1; human cytomegalovirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2545
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The minimal promoter PhCMV*-1 is based on the human CMV intermediate-early promoter (with enhancer region removed), fused to a tetracycline operator, teto. The promoter is used to express tTA transactivator in host cells. In clone pullb BGR3 (given in Q76269), CDNA for rabbit progesterone receptor is under the control of PhCMV*-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Buldard H, Gossen M;
WPI; 95-392612/50.
Polynucleotide encoding trans:activator fusion protein contg. tet
repressor - used to control expression of gene regulated by minimal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric
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(GOSS/) GOSSEN M.
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Local Similarity 66.3%;
hes 128; Conservative
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; US-076726.
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0; M
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                                                                                                              No. 2.42e-25;
Mismatches 65;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Mon Nov 2 16:27:57 1998; MasPar time 27.56 Seconds 702.514 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score:

>US-08-906-365-2 (1-530) from US08906365.pep 3904 1 MDIKNSPSSINSPSSYNCSQ.....ECSPAEDSKSKEGSQNPQSQ 530

Scoring table: PAM 150 Gap 11

Searched: 120441 segs, 36531193 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir56 1:pir1 2:pir2 3:pir3 4:pir4 5:nrl3d

Statistics: Mean 48.751; Variance 99.595; scale 0.489

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	Result No.
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X rec	retinoic acid recepto		retinoic acid recepto	rec	on II	retinoic acid recepto	retinoid X receptor b	glucocorticoid recept	androgen receptor - c	humanCHICKEN ESTROGEN	androgen receptor B -	humanCHICKEN ESTROGEN	humanCHICKEN ESTROGEN	humanCHICKEN ESTROGEN	mineralocorticoid rec	androgen receptor A -	receptor -	androgen receptor - r	androgen receptor - m	glucocorticoid recept	estrogen receptor - b
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ALIGNMENTS

174 KRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRERCGYRLVRRQR 233	174	Qγ
	121	д
114 EHTLPVNRETLKRKVSGNRCASPVTGPGSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFF 173	114	Qy
61 EHTLPVNRETLKRKVSGNRCASPVTGPGSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFF 120	61	망
54 MNYSIPSNVINLEGGPGRQTTSPNVLWPTPGHLSPLVVHRQLSHLYAEPQKSPWCEARSL 113	54	Qy
1 MNYSIPSNYTNLEGGPGRQTTSPNYLWPTPGHLSPLYVHRQLSHLYAEPQKSPWCEARSL 60	1	망
y Match 90.5%; Score 3532; DB 2; Length 477; Local Similarity 100.0%; Pred. No. 0.00e+00; hes 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match Best Local Matches 4	
#leng	SUMMARY	JS
96,99,113,116 #binding_site zinc (Cys) #status predicted\ 132.138.148.151 #binding site zinc (Cys) #status predicted\	96,99,113, 132,138,14	
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	167-182	
#region zinc finger CCCC	132-156	
333 #region zinc finger CCCC motif\	96-116	
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-	KEYWORDS	Z.
FICATION #superfamily estrogen receptor; erbA transforming protein	CLASSIFICATION	ū
#cross-reference		
##residues 1-477 ##label MOS	##resid	
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216,222,232,235
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##cross-references GB:L20735
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##residues 1-58
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YSSASLSYAASSETFG-SSSLTGLHT-LNNVPPSSPVVFLAKLPQLSPFIHHHGQQVPYYL 127
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                                                                                    h 44.4%;
Similarity 50.8%;
247; Conservative
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N #superfamily estrogen re
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#formal_name Xenopus laevis #common_name African clawed
28-reb-1992 #sequence_revision 14-Jul-1994 #text_change
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steroid hormone receptor; transcrip
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#region zinc finger CCCC motif\
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Pred. No. 0.00e+00;
112; Mismatches 107;
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#title
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Greene, G.L.; O'Malley,
#journal Mol. Endocrinol. (1987) 1:
#title : Structural organization an
estrogen receptor.
#cross-references_MVID:88318621
                                                                                                                                                                                                                                                                                                                                                                         #accession
##status
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#accession S07192
                                                                                                                                                                                                                                                                                                         #authors
##residues
1-256,/E/,258-589 ##label KRU
##cross-references EMBL:X03805; NID:g63378; PID:g63380
##cross-references EMBL:X03805; NID:g63378; PID:g63380
NT The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues.

**YT In the absence of ligand, steroid hormone receptors are thought be weakly associated with nuclear components; hormone binding greatly increases receptor affinity. The hormone-receptor appears to recognize discrete DNA sequences upstream of transcriptional start sites.
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                                                                                                                                                                                                                                        Krust, A.; Green, S.; Argos, P.
Bornert, J.M.; Chambon, P.
EMBO J. (1986) 5:891-897
The chicken oestrogen receptor
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#formal_name Gallus gallus #common_name chicken
06-Mar-1992 #sequence_revision 14-Jul-1994 #text_change
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ey, B.W.
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Local Similarity 51.6%;
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                                                                                                                                                                                                QRHUE #type complete
estrogen receptor 1 - human
ER1; estrogen receptor alpha
#formal_name Homo sapiens #common_name man
28-May-1986 #sequence_revision 28-May-1986 #text_change
                                             Science (1986) 231:1150-1154
Sequence and expression of human estrogen receptor
                                                                                                          Greene, G.L.; Gilna,
                                                                                                                                                                   A94284; A93376; A43021; S27143;
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finger
                 complementary DNA.s MUID:86122927
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#domain DNA binding #status predicted homology #label ERBA\
#domain erbA transforming protein homology #label ERBA\
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Pred. No. 0.00e+00;
112; Mismatches 99
                                                                                                                                                   D41925
                                                                                                          P.; Waterfield,
                                                                                                                                                                   S34000; A41925;
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homology to v-erb-A.
#cross-references MUID:86146892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##status preliminary
##molecule_type mRNA
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##cross-references GB:M12674;
                                                                                                                                                                                                                ##molecule_type mRNA
##cross-references GB:M69296
                                                                                                                                                                                                                                                                                                                                             ##note
                                                                                                                                                                                                                                                                                                                                                                                                          ##residues 1-214,'ELPTLC' ##label DOT ##cross-references GB:M69297; NID:g182218; PID:g182219 ##experimental_source clone 4; breast cancer
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##cross-references GB:X03635; NID:g31233;
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                                                                                                                                               ##note sequence extracted from NCBI backbone (NCBIN:106597)
The steroid hormones and their receptors are involved in the
                                                                                                                                                                                            ##experimental_source clone 24; breast cancer
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regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues.

n the absence of ligand, steroid hormone receptors are thought be weakly associated with nuclear components; hormone binding greatly increases receptor affinity. The hormone receptor components to recognize discrete DNA sequences upstream of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A41925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dotzlaw, H.; Alkhalaf, M.; Murphy, L.C. Mol. Endocrinol. (1992) 6:773-785
Characterization of estrogen receptor variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ponglikitmongkol, M.; Green, S.; Chambon, P. EMBO J. (1988) 7:3385-3388
Genomic organization of the human oestrogen receptor A43021
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Estrogen receptor variant messenger RNA lacking exon 4
estrogen-responsive human breast cancer cell lines.
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Sequence analysis of the 5' flanking
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                                                                                                                                                                                                                                                                                                the complete sequence of neither the nucleotide nor the protein is shown in this paper sequence extracted from NCBI backbone (NCBIN:106580)
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'P',462-467;508-528 ##label PON
                                                                                                                                                                                                                                                          significant sequence differences
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NID:g182192; PID:g182193
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##molecule_type mRNA
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##cross-references and their receptors are invol
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                                                                                                                                                                                                                                                                                                                                  QRMSE #type complete
estrogen receptor - mouse
#formal_name Mus musculus #common_name house mouse
05-Mar-1992 #sequence_revision 14-Jul-1994 #text_change
05-Sep-1997
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151/2; 215/1; 254/1; 366/1; 412/2; 457/1; 518/2
                                                                                                                                                                                                                                                White, R.; Lees, J.A.; Needham, M.; Ham, Mol. Endocrinol. (1987) 1:735-744
                                                                                                                                                                                                                        Structural organization
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#domain erbA transforming protein homology #label ERBA\
#region zinc finger CCCC motif\
#region zinc finger CCCC motif\
#region zinc finger CCCC motif\
#common steroid binding #status predicted #label STB\
#binding_site phosphate (Ser) (covalent) #status
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e expression and affect
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                                                                                                                                                                                                                           EHLYNMKCKNVVPLYDLLLEMLDAHRLHAPASRMGVPPEEPSQTQLATTSSTSAHS
                                                                                                                                                                                                                                                                                               TATQDA-DSSRKLAHLLNAVTDALVWVIAKSGISSQQQSMRLANLLMLLSHVRHASNKGM
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L,241,244
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Similarity 51.7%;
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n the absence of ligand, steroid hormone receptors are thought to be weakly associated with nuclear components; hormone binding greatly increases receptor affinity. The hormone-receptor complex appears to recognize discrete DNA sequences upstream of transcriptional start sites.
ORRIE #type complete
estrogen receptor - rat
#formal_name Rattus norvegicus
30-Sep-1991 #sequence_revision
05-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA binding; nucleus;
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#region zinc finger CCCC motif\
#region zinc finger CCCC motif\
#region nuclear location signal\
#domain steroid binding #status predicted #label
#binding_site zinc (Cys) #status predicted\
#binding_site zinc (Cys) #status predicted\
#binding_site phosphate (Ser) (covalent) #status
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h 599 #mol
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Pred. No. 0.00e+00;
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eptor; transcription
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14-Jul-1994 #text_change
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Koike, S.; Sakai, M.; Muramatsu, M. Nucleic Acids Res. (1987) 15:2499-2513

Molecular

cloning

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\$07379; \$16731 \$07379

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FEATURE
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190,193,207,210
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241,310
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188-461
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224-246
261-276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ##cross-references EMBL:X61098; NID:g56120; PID:g56121
The steroid hormones and their receptors are invo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                          SSTLKSLEEKDHIHRVLDKINDTLIHLMAKAGLTLQQQHRRLAQLLLILSHIRHMSNKGM 527
                                                                                                                                                                LFAPNLLLDRNQGKCVEGMVEIFDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGYYTFL 467
                                                                                                                                                                                                                                                                 MGLLTNLADRELVHMINWAKRVPGFGDLNLHDQVHLLECAWLEILMIGLVWRSMEHPGKL 407
                                                                                                                                                                                                                                                                                                                                                            ATNOCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRERCGYRLVRRQRSADE-QLHCA-GK 244
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EHLYNMKCKNVVPLYDLLLEMLDAHRLHAPASRMGVPPEEPSQSQLTTTSSTSAHS
                                            TATQDA-DSSRKLAHLLNAVTDALVWVIAKSGISSQQQSMRLANLLMLLSHVRHASNKGM
                                                                                                                                       IFAPDLYLDRDEGKCVEGILEIFDMLLATTSRFRELKLQHKEYLCVKAMILLNSSMYPLV
                                                                                                                                                                                                                                     MMSLTKLADKELVHMISWAKKIPGFVELSLFDQVRLLESCWMEVLMMGLMWRSIDHPGKL
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In the absence of ligand, steroid hormone receptors are thought to be weakly associated with nuclear components; hormone binding greatly increases receptor affinity. The hormone-receptor complex appears to recognize discrete DNA sequences upstream of transcriptional start sites.
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#domain erbA transforming protein homology #label ERBA\
#region zinc finger CCCC motif\
#region zinc finger CCCC motif\
#region zinc finger CCCC motif\
#region nuclear location signal\
#domain steroid binding #status predicted\
#binding_site zinc (Cys) #status predicted\
#binding_site zinc (Cys) #status predicted\
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183-456
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#title The C-terminal half of the porcine estradiol receptor contains no post-translational modification: determinations references MUID:95080454
#accession 147140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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##restitues 297-307;310-313;320-323;329-332;337-340;417-420;466-473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 SPSPLVLLHPPPQLSPFLHPHGQQVPYYLENEPSGY-AVREAGPPAFYRPNSDNRRQGGR 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ##status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ##molecule_type mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                         73 TTSPNVLWPTPGHLSP-LVVHRQLSHLYAEPQKSPWCEARSLEHTLPVNRETLKRKVSG- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                    NRCASPV-TGP-G--SKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICP
                                                                                                                    MGLLINLADRELVHMINWAKRVPGFLDLSLHDQVHLLECAWLEILMIGLVWRSMEHPGKL 402
                                                                                                                                                                                                                                     KA-KRSGG--HAPR-VRELLLDA--LS--PEQLVLTLLEAEPPHVLIS-RPSAPFTEASM
                                                                                                                                                                                                                                                                                                                                                                                           ERLASTSDKGSMAMESAKETRYCAVCNDYASGYHYGVWSCEGCKAFFKRSIQGHNDYMCP 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HILLNMKCKNVVPVYDLLLEMLNAHVLRGCKSSITGSECSPAEDSKSKEGSQNPQS
EHLYNMKCKNVVPLYDLLLEMLDAHRLHA 551
                               TATQDA-DSSRKLAHLLNAVTDALVWVIAKSGISSQQQSMRLANLLMLLSHVRHASNKGM
                                                               SSTLKSLEEKDHIHRVLDKITDTLIHLMAKAGLTLQQQHRRLAQLLLILSHFRHMSNKGM
                                                                                                                                                                                                                                                                   PGDMRSANLWPSPLLIKHTKKNSPVLSLTADQMISALLEAEPPIIYSEYDPTRPLSEASM 342
                                                                                                                                                                                                                                                                                                   ATNQCTIDKNRRKSCQACRLRKCYEVGMMKGGIRKDRRGGRMLKHKRQRDDGEGRNEAVP
                                                                                                 IFAPDLYLDRDEGKCVEGILEIFDMLLATTSRFRELKLQHKEYLCVKAMILLNSSMYPLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 42.4%;
Similarity 53.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     porcine estradiol receptor by restricted $66250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thole, H.H.; Maschler, I.; Jungblut, P.W. Eur. J. Biochem. (1995) 231:510-516 Surface mapping of the ligand-filled C-terminal half of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \begin{tabular}{ll} \tt #superfamily estrogen receptor; erbA transforming \\ homology \end{tabular} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            estradiol receptor - pig
#formal_name Sus scrofa domestica #common_name domestic
21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #domain erbA transforming protein homology #label ERBA
#length 595 #molecular-weight 66361 #checksum 5521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 steroid hormone receptor; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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eceptor - pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1654; DB 2;
Pred. No. 5.58e-303;
97; Mismatches 90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NID:g587554; PID:g587555
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##1esiques 1-574 ##label ##cross-references GB:M31559 REFERENCE A40070
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Best Local Similarity 56.3%;
                                                                                                                                                                                                                                                                                                                                                145-421
147-167
183-207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #journal #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #journal Mol. Endocrinol. (1989) 3:44-51
#title Identification and estrogen induction of two
receptors (ER) messenger ribonucleic acids
trout liver: sequence homology with other E
#cross-references MUID:89127284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #accession
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       estrogen receptor cDNA.
#cross-references_MUID:91006824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #authors
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   427
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                                                368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ##molecule_type mRNA
##residues 150-574 ##label PA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ##molecule_type mRNA
##residner
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                                            HMIAWAKKVPGFQELSLHDQVQLLESSWLEVLMIGLIWRSIHCPGKLIFAQDLILDRSEG
AHLLNAVTDALVWVIAKSGISSQQQSMRLANLLMLLSHVRHASNKGMEHLLNMKCKNVVP
             ESMLDNITDALIHHISHSGASVQQQPRRQAQLLLLLSHIRHMSNKGMEHLYSIKCKNKVP 500
                                                                                             HMISWAKKIPGFVELSLFDQVRLLESCWMEVLMMGLMWRSIDHPGKLIFAPDLYLDRDEG
                                                                                                                                            RVREL--LLDA-LS-PEQLVLTLLEAEPPHVLISRPS-A-PFTEASMMMSLTKLADKELV
                                                                                                                                                        SLNGGGGWRGPRITMPPEQVLFLLQGQTP-ALCSRQKVARPYTEVTMMTLLTSMADKELV 320
                                                                                                                                                                                        RLRKCYEVGMVKCGSRRERCGYRLVRRQ-R---SA-D-EQLHCA-GKAKRS--GGH--AP 253
                                                                                                                                                                                                       RLRKCYEVGMVKGGLRKDRGG-RVLRKDKRYCGPAGDREKPTVTWSTGQRPQDGGRNSSS 261
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                                                                                                                                                                                                                                                                                                                                  #region zinc finger\
#region zinc finger
#length 574 #molecular-weight 62871 #checksum
                                                                                                                                                                                                                                                                                                                                                                                                                  #superfamily estrogen receptor;
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Mol. Cell. Endocrinol. (1
Full-length sequence and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pakdel, F.; Le Guellec,
Valotaire, Y.
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A37197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A37197 #type complete estrogen receptor - rainbow trout #formal_name Oncorhynchus mykiss #common_name rainbow trout 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 08-Sep-1997
                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              zinc
                                                                                                                                                                                                                                                                                    Score 1516;
Pred. No. 1.6
78; Mismatch
                                                                                                                                                                                                                                                                                                                                                                    transforming
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                                                                                                                                                                                                                                                                                                                                                                                              finger
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1.66e-274;
75;
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erbA transforming
                                                                                                                                                                                                                                                                                                           Length 574;
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#journal
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#authors
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103-382
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Best Local S
Matches 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##residues 1-535 ##label ROG
##cross-references EMBL:X89959; NID:g929901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ##molecule_type mRNA
##residues 1-53
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:|||||||:||::|:::|:::|:::|:
VYDLLLEMLNAHYLRGC-KSSITGSEC-SPAEDSKSKEGS 524
VPVYDLLLEMLNAHVLRGC-KSSITGSEC-SPAEDSKSKEGS
                                VPLYDLLLEMLDGHRLQSPGKVAQAGEQTEGPSTTTTTSTGS
                                                                                                  AVESMLDNITDALIHHISHSGASVQQQPRRQVQLLLLLSHIRHMSNKGMEHLYSIKCKNK
                                                                                                                                                        EGDCVEGMAEIFDMLLATVSRFRMLKLKPEEFVCLKAIILLNSGAFSFCSNSVESLHNSS
                                                                                                                                                                                                       LVHMISWAKKIPGFVELSLFDQVRLLESCWMEVLMMGLMWRSIDHPGKLIFAPDLVLDRD
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                                                                                                                                                                                                                                                                                                                                                                 RLRKCYEVGMVKGG1RKDRGG-RVLRKDKRYCGPAGDREKPYGD1EHRTAPPQDGGRNSS 219
                                                                  KLAHLLNAVTDALVWVIAKSGISSQQQSMRLANLLMLLSHVRHASNKGMEHLLNMKCKNV
                                                                                                                                    EGKCVEGILEIFDMLLATTSRFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDA-DSSR
                                                                                                                                                                                                                                                                                                           SSSLSGGGGWCGPRITMPPEQVLFLLQGAEPPALCSRQKVARPYTEVTMWTLLTSMADKE 279
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Wigham, T.
submitted to t
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oestrogen receptor - Atlantic salmon (fragment)
#formal_name Salmo salar #common_name Atlantic salmon
13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change
31-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #domain erbA transforming
#length 535 #checksum 9963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         steroid
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55.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1503; DB 2;
Pred. No. 7.90e-272;
75; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL Data Library, July 1995
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erbA transforming
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524
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Nucleic Acids F A novel 80 kDa

Res. (:

estrogen receptor

containing

(1996)

24:962-969

Pink,

J.J.;

Wu,

S.Q.; Wolf, D.M.; Bilimoria,

м. М.

Jordan,

\$64737 #type complete 80K estrogen receptor - human #formal_name Homo sapiens #common_name man 28-oct-1996 #sequence_revision 13-Mar-1997

#text_change

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ACCESSIONS
REFERENCE
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Library, January 1996
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 327
                                                                                                                                                                                             446 ISSQQQSMRLANLLMLLSHVRHASNKGMEHLLNMKCKNVVPVYDLLLEMLNAHV
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                                  272
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                                                                                                                                                             161 MKCLKVGMLKEGVRLDRV--R-GGRQKY-KRRLDSENSPYLNLPISPPAKKPLTKIVS-N 215
                                                                                                                                                                                                                                                                                                                                                                                                                                               ##residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type mRNA
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|: ||:| |||:|::|:: ||: || :| || ::| : : | |:|::: :| |
QVRLLESCWMEVLMMGLMWRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFDMLLATTSR
                           QMSLLQSAWMEILILGIVYRSLPYDDKLAYAEDYIMDEEHSRLV-GLLDLYRAILQLVRR 330
                                                               QLVLTLLEAEPPHVLISRPSAPFTEASMMMSLTKLADKELVHMISWAKKIPGFVELSLFD 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QMSLLQSAWMEILILGIVYRSLPYDDKLAYAEDYIMDEEHSRLV-GLLELYRAILQLVRR 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QLVLTLLEAEPPHVLISRPSAPFTEASMMMSLTKLADKELVHMISWAKKIPGFVELSLFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MKCLKVGMLKEGVRLDRV--R-GGRQKY-KRRLDSENSPYLSLQISPPAKKPLTKIVS-- 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLCLVCGDIASGYHYGVASCEACKAFFKRTIQGNIEYSCPATNECEITKRRKKSCQACRF 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVRLLESCWMEVLMMGLMWRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFDMLLATTSR
                                                                                             -L-LGV-EQDKLYAM-PPNDIPEGDIKALTTLCELADRELYFLINWAKHIPGFPSLTLGD 271
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                                                                                                                              RKCYEVGMVKCGSRRERCGYRLVRRQRSADEQLHCAGKAKRSGGHAPRVRELLLDALSPE 266
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                                                                                                                                                                                                                                                         20.5%;
1 Similarity 38.7%;
137; Conservati
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estrogen receptor related protein - mouse
#formal_name Mus musculus #common_name house mouse
13-Jan-1996 #sequence_revision 01-Mar-1996 #text_ch
31-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Expression of a novel member of estrogen response element-binding nuclear receptors is restricted early stages of chorion formation during mouse
                                                                                                                                                                                                                                                                                                                                                                                steroid hormone receptor; zinc finger
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S58087
                                                                                                                                                                                                                                                                                                                               #length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pettersson,
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                                                                                                                                                                                                                                                                                                                               #domain erbA transforming protein homology #label
rth 433 #molecular-weight 48400 #checksum 1075
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Pred. No. 1.97e-128;
85; Mismatches 110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mattsson,
                                                                                                                                                                                                                                                                                             Length 433;
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445 GISSQQQSMRLANLLMLLSHVRHASNKGMEHLLNMKCKNVVPVYDLLLEMLNA

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REFERENCE A49074
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                                                                                                                                                                                                                                                                                                                                                            Query Match 20.5%;
Best Local Similarity 39.9%;
Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       174-434
176-196
212-236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #journal #title
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #authors Giguere, V.; Yang, N.; & #journal Nature (1988) 331:91-94 #title Identification of a new #cross-references MUID:88122546 #accession A29345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #authors
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##residues 166-169,'X',171-173 ##label
                 466
                                                385
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                                                                                                                                                                                                                                                                                                                RLCLVCGDVASGYHYGVASCEACKAFFKRTIQGSIEYSCPASNECEITKRRRKACQACRF
                                                                                                                           SDQMSVLQSVWMEVLVLGVAQRSLPLQDELAFAEDLVLD-EEGARAAGLGELGAALLQLV
                                                                                                                                                                                        TKCLRVGMLKEGVRLDRVRGGRQKYKRRPEVDPLPFPG-P-FPAGPLAVAGGPRKTAAPV 291
                                                                                                                                                                                                                                                                                               HFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRL 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YKKLKVEKEEFMILKALALANSDSMY--I---ENLEAVQKLQDLLH----EALQ-DYELS-
              GPGGGAERRRAGRULLTUPLURQTAGKVLAHFYGVKLEGKVPMHKUFLEMLEA
                                              SRFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDADSSRKLAHLLNAVTDALVWVIAKS
                                                                           RRLQALRLEREEYVLLKALALANSDSVHIEDEPRLWSSCEKLLH--EAL---LEYEAGRA
                                                                                                         FDQVRLLESCWMEVLMMGLMWRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFDMLLATT
                                                                                                                                                                      EQLVLTLLEAEPPHVL-ISRPSAPFTEASMMSLTKLADKELVHMISWAKKIPGFVELSL
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steroid hormone receptor ERR1 precursor - human
estrogen-related receptor
#formal_name Homo sapiens #common_name man
15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change
12-Sep-197-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #superfamily unassigned erbA-related
    transforming protein homology
    DNA binding; nucleus; steroid hormone
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SV40 early-to-late switch invo
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                                                                                                                                                                                                                                                                                                                                                                                                                     #length
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#region
gth 521
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#molecular-weight 55742
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Pred. No. 1.
74; Mismatci
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L.24e-12
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                                                                                                                                                                                                                                                                                                                                                            128;
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                                                                                                                                                                                                                                                                                                                                                                                                                       #checksum
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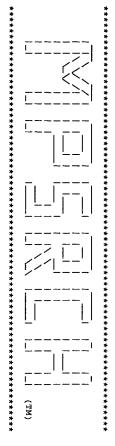
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FEATURE
555-819
557-577
593-617
                ACCESSIONS
REFERENCE
                                                                                       TITLE
ORGANISM
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #journal Schott, D.R.; Shyamala, G.; Schneider, #journal Biochemistry (1991) 30:7014-7020 #title Molecular cloning, sequence analyses, a complementary DNA encoding murine pro #cross-references MUID:91299759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
 #authors
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1-923 ##label SCH
##cross-references GB:M68915; GB:J05333; NID:g200471; PID:g200472
##cross-references GB:M68915; GB:J05333; NID:g200471; PID:g200472
                                                                                                                                                                                                                                  838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##status
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Local Similarity 30.8%;
nes 123; Conservative
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                                                                                                                                                                                                                                                                                        E-LSFYSLCLTMWQIPQEFVKLQVTHEEFLCMKVLLLLNT-I-PLEGLRSQSQFEEMRSS
                                                                                                                                                                                                                                                                                                                                          KKIPGFVELSLFDQVRLLESCWMEVLMMGLMWRSIDH-PGKLI-FAPDLVLDRDEGKCVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTPGHLSPLVVHRQLSHLYAEPQKSPWCEARSLEHTLP-VNRETLK-RKVSGNRCASPVT 138
                                                                                                                                                                                                                                YIRELIKAIG-LRQKGVVPTSQRFYQLTKLLDSLHDLVKQ 876
                                                                                                                                                                                                                                                                      GILEIFDM-L-L-ATTSRFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDADSSRKLAH
                                                                                                                                                                                                                                                                                                                                                                            KSLPGFRNLHIDDQITLIQYSWMSLMVFGLGWRSYKHVSGQMLYFAPDLILN-EQ-R-MK 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSPNQEIQLVP-PLINLLMSIEPDVIYAGHDNTKPDTSSSLLTSLNQLGERQLLSVVKWS 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPGSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRR 198
                                                                                                                                                                                                                                                                                                                                                                                                                 -ELLLDA-LSPEQLVLTLLEAEPPHVLISRPSA-PFTEASMMSLTKLADKELVHMISWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KSCQACRIRKCYEVGMVKCGSRRERCGYRIVRRQRSADE-Q1-HCAGKAKRSGGHAPRVR 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KNCPACRLRKCCQAGMVL-GGRKFK-KFNKVRVMRTLDGVALPQSVGLPNESQALSQRIT 664
                                          #type complete
progesterone receptor - rat
#formal_name Rattus norvegicus #
02-Aug-1996 #sequence_revision 0
25-Apr-1997
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A39596
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#region zinc finger
#length 923 #molecular-weight 99073
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progesterone receptor B form - mouse
#formal_name Mus musculus #common_name house mouse
20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change
31_Oct-1997
                I53280; B23733;
I53280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA binding; nucleus; steroid regulation; zinc finger
Park-Sarge, O.K.; Mayo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #domain erbA transforming
#region zinc finger\
#region zinc finger
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Pred. No. 6.28e-105;
112; Mismatches 138;
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                                                                  #common_name Norway rat
02-Aug-1996 #text_change
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CLASSIFICATION #superfamily progr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #title Transient expression of progesterone receptor messenger RNA in ovarian granulosa cells after the preovulatory ecross-references MUID:92049379
#accession B23733
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 17.2%;
Best Local Similarity 32.6%;
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #cross-references MUID:94130817
#accession I53280
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                                                                                                                                                                                                                                                                                                                                616
                                                                                                                                                                                                                                                                                                                                                              674 VP-PLINLLMSIEPDVVYAGHDNTKPDTSSSLLTSLNQLGERQLLSVVKWSKSLPGFRNL 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ##molecule_type mRNA

##residues 555-589,'W',591-624;742-910 ##label PAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              **status preliminary; translated from GB/EMBL/DDBJ
*#molecule_type mRNA
##rosiding
                      847 G-LRQKGVVPSSQRFYQLTKLLDSLHDLVKQ 876
: |: ::| |: :|:|| | |::
                                                                         380
                                                                                                             789
                                                                                                                                                323
                                                                                                                                                                                  733
                                                                                                                                                                                                                208 KCYEVGMVKCGSRRERCGYRLVRRQRSADE-QL-HCAGKAKRSGGHAPRVR-ELLLDA-L 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L-L-ATTSRFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDADSSRKLAHLLNAVTDAL 437
                                                                                                       LTMWQIPQEFVKLQVTHEEFLCMKVLLLLNT-I-PLEGLRSQSQFEEMRSSYIRELIKAI 846
                                                                                                                                                                                                                                                                                                                        KCCQAGMVL-GGRKFK-KFNKVRVMRALDGVALPQSVAFPNESQTLGQRITFSPNQEIQL 673
VWVIAKSGISSQQQSMRLANLL-MLLSHVRH 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #domain erbA transforming protein homology #label ERBA\
#region zinc finger\
#region zinc finger
#length 923 #molecular-weight 99407 #checksum 9843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA binding; nucleus; steroid hormone receptor; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endocrinology (1994) 134:709-718
Regulation of the progesterone receptor gene by gonadotropins and cyclic adenosine 3',5'-monophosphate in rat granulosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 671; DB 2; Length 923;
Pred. No. 5.99e-103;
94; Mismatches 108; Indels 21; Gaps
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Search completed: Mon Nov 2 16:30:48 1998 Job time: 171 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Nov 2 16:32:21 1998; MasPar time 40.39 Seconds 653.369 Million cell updates/sec

Tabular output not generated.

rfect Score: >US-08-906-365-2 (1-530) from US08906365.pep 3904 1 MDIKNSPSSINSPSSYNCSQ.....ECSPAEDSKSKEGSQNPQSQ 530

Scoring table: PAM 150 Gap 11

Searched:

165420 seqs, 49795644 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb16
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mamma1 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Mean 49.103; Variance 84.403;

scale 0.582

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	DB	IJ	ţţ	Pred. No.
–	3564	91.3	549	11	035784	OESTROGEN RECEPTOR BET	0.00e+00
2	3532	90.5	477	4	Q92731	ESTROGEN RECEPTOR BETA	
ω	3480	89.1	513	4	060685	ESTROGEN RECEPTOR BETA	0.00e+00
4	3476	9	495	4	809090	ESTROGEN RECEPTOR BETA	0.00e+00
տ	3278	84.0	485	11	008537	RECEPTOR	
თ	3274	83.9	485	11	Q62986	ESTROGEN RECEPTOR BETA	
7	3250	٠	485	11	035635	ESTROGEN RECEPTOR, SUB	3 0.00e+00
œ	3089	•	503	11	035785	OESTROGEN RECEPTOR BET	0.00e+00
9	3076		503	11	070195	ESTROGEN RECEPTOR BETA	1 0.00e+00
10	2545	65.2	446	11	055015	ESTROGEN RECEPTOR BETA	0.00e+00
11	2347	60.1	464	11	055016	ESTROGEN RECEPTOR BETA	1 0.00e+00
12	2240	57.4	573	13	013012	ESTROGEN RECEPTOR.	0.00e+00
13	1701	43.6	587	3	Q91250	ESTROGEN RECEPTOR.	0.00e+00
14	1473	37.7	701	4	Q13511	80 KDA ESTROGEN RECEPT	0.00e+00
15	1227	31.4	307	13	091424	ESTROGEN RECEPTOR (FRA	1.08e-255
16	938	24.0	276	13	042174	ESTROGEN RECEPTOR (FRA	1 6.93e-186
17	816	20.9	481	4	Q14514	ESTROGEN RECEPTOR-RELA	1.
18	799	٠	433	11	Q61539	ESTROGEN RECEPTOR RELA	1.
19	765	19.6	159	σ	046402	ESTROGEN RECEPTOR ALPH	1 1.30e-144
20	760	19.5	420	11	008580	ESTROGEN RECEPTOR RELA	2.00e-

4.4 5	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21
461 461	471	480	4.88	490	494	495	500	508	512	529	532	543	557	5/70	572	582	589	599	617	639	671	692	754
11.8	12.1	12.3	12.5	12.6	12.7	12.7	12.8	13.0	13.1	13.6	13.6	13.9	14.3	14.6	14.7	14.9		15.3	15.8	16.4		17.7	19.3
535	598	386	385	412	441			414	807	348	125	344	336	901	730	659	795	789	778	360	923	105	159
4 U	11	13	13	13	3	13	11	u	13	13	σ	13	4	11	4	13	11	13	σ	13	11	σ	σ
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RETINOID X RECEPTOR. TINUR= NGFI-B/NUR77 BE	ORPHAN NUCLEAR HORMONE	ORPHAN NUCLEAR RECEPTO	NUCLEAR RECEPTOR TLX.	RETINOID X RECEPTOR BE	RETINOID X RECEPTOR AL	RETINOID X RECEPTOR.	MTLL=TAILLESS HOMOLOG.	RETINOID X RECEPTOR.	GLUCOCORTICOID RECEPTO	PROGESTERONE RECEPTOR	ESTROGEN RECEPTOR ALPH	ANDROGEN RECEPTOR (FRA	ESTROGEN RECEPTOR-RELA	RAT ANDROGEN RECEPTOR.	ANDROGEN RECEPTOR.	PROGESTERONE RECEPTOR.	GLUCOCORTICOID RECEPTO	ANDROGEN RECEPTOR ALPH	GLUCOCORTICOID RECEPTO	PROGESTERONE RECEPTOR	PROGESTERONE RECEPTOR.	ESTROGEN RECEPTOR BETA	ESTROGEN RECEPTOR (FRA
7.57e-74 7.57e-74	4.06e-76	.63e	5.44e-80	1.90e-80	2.32e-81	1.37e-81	4	1.45e-84	1.76e-85	2.18e-89	4.45e-90	1.30e-92	7.59e-96	7.43e-99	2.55e-99	1.22e-101	2.89e-103	1.37e-105	8.74e-110	6.33e-115	1.99e-122	2.30e-127	5.26e-142

ALIGNMENTS

	80 STSNLDGGPVRQSTSPNVLWPTSGHLSPLATHCQSSLLYAEPQKSPWCEARSLEHTLPVN 139 : : : :	рь
	Y 1 MDIKNSPSSINSPSSYNCSQSILPLEHGSIYIPSSYVDSHHEYPAMTFYSPAVMNYSIPS 60	Qy
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0,	Query Match 91.3%; Score 3564; DB 11; Length 549; Best Local Similarity 88.3%; Pred. No. 0.00e+00; Matches 468; Conservative 43; Mismatches 19; Indels 0; Gaps	~ ~ ~
	SEQUENCE 549 AA; 61325 MW; 7FB319E5 CRC32	SQ
	T CONFLICT 184 184 P -> S (IN REF. 2).	3 3
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	R PFAM; PFUGIOS; z1-C4. RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN;	K R
	PFAM; PF00104; hormone_rec.	DR
	PROSITE: PS00031	뮸
	R EMBL; AJUUZ6UZ; ELZ8/358;	DR E
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	BROWN T.A.;	RA :
	PETERSEN D.N., TKATCEVIC G.T., KOZA-TAYLOR P.H., TURI T.G.,	R Z
		R R
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	STRAIN=WISTAR: TISSUE=PROSTATE:	25
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	EUTHERIA; RODENTIA.	8
	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	88
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Best Local
Matches 4
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Q92731;
                                                                                                                                                                                                       MOSSELMAN S., POLMAN J., DIJKEMA R.;
FEBS LETT. 392.49-53(1996).
FEBS LETT. 392.49-53(1996).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)
EMBL; X99101; E25390; -.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
PFAM; PF00104; hormone_rec.
PFAM; PF00105; zf-c4.
RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING;
ZINC-FINGER.
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EUKARYOTA; METAZOA; C
EUTHERIA; PRIMATES.
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01-FEB-1997 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
ESTROGEN RECEPTOR BETA.
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SADEQLHCAGKAKRSGGHAPRVRELLLDALSPEQLVLTLLEAEPPHVLISRPSAPFTEAS
                   KRSIQGHNDYICFATNQCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRERCGYRLVRRQR
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Similarity 100.0%;
477; Conservative
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                                                                                                                                                   Score 3532; DB 4;
Pred. No. 0.00e+00;
0; Mismatches 0
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Best Local S
Matches 47
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1. SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

EMBL; APO60555; G3091286; PROSITE; PSG0031; NUCLEAR, RECEPTOR; 1.

RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR LINC-FINGER.
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01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATIC
ESTROGEN RECEPTOR BETA 3 ISOFORM.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA;
EUTHERIA; PRIMATES.
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Local Similarity 97.7%;
hes 470; Conservation
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VLDRDEGKCVEGILEIFDMLLÄTTSRFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDA
                             VLDRDEGKCVEGILEIFDMLLATTSRFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDA
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07, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDAT
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1. No. 0.00e+00;
Mismatches 3
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008537;
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EMBL; AF051428; G2961559; -.

PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.

RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING; NI
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060608;
01-AUG-1998 (TREMBLREL. 07, CREATED)
01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
ESTROGEN RECEPTOR BETAZ SPLICE VARIANT.
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EUKARYOTA; METAZOA;
EUTHERIA; PRIMATES.
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Pred. No. 0.
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DNA-BINDING;
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062986 PRELIMINARY;
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01-NOV-1996 (TREMBLREL. 0
01-NOV-1996 (TREMBLREL. 0
01-JUN-1998 (TREMBLREL. ESTROGEN RECEPTOR BETA. RATTUS NORVEGICUS (RAT).
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EMBL; U81451; G1912468;
MGD; MGI:109392; ESTRB.
PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
PFAM; PF00104; hormone_rec.
PFAM; PF00105; zf-c4.
RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING;
ZINC-FINGER.
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ESTRB.
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01-JUL-1997 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
ESTROGEN RECEPTOR BETA.
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EUKARYOTA; METAZOA;
EUTHERIA; RODENTIA.
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NATURE 11:353-365(1997).
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TREMBLAY G.B.,
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Similarity 88.9%;
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                                                         PRELIMINARY;
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Pred. No. 0.00e+00;
34; Mismatches 20;
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Matches 43
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KUIPER G.G.J.M., ENMARK E., PELTO-HUI
GUSTAFSSON J.A.;
PROC. NATL. ACAD. SCI. U.S.A. 93:5925
-!- SUBCELLULAR LOCATION: NUCLEAR (BY
EMBL; U57439; G1373281; --
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1
                                                                                035635;
035635;
01-JAN-1998
01-JAN-1998
01-AUG-1998
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EUTHERIA; I
[1]
                                                     ESTROGEN RECEPTOR, SUMUS MUSCULUS (MOUSE), EUKARYOTA; METAZOA;
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PFAM; PF00105; zf-C4.

RECEPTOR; TRANSCRIPTION REGULATION;
ZINC-FINGER.
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SEQUENCE FROM N.A.

PETTERSSON K., GRANDIEN K., KUIPER G.G., GUSTAFSSON C

SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
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                                            EUTHERIA;
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YRLVRRQRSADEQLHCAGKAKRSGGHAPRVRELLLDALSPEQLVLTLLEAEPPHVLISRP
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l Similarity 88.7%;
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                                                                       (TREMBLREL. 05, CREATED)
(TREMBLREL. 05, LAST SEQUENCE UPDATE)
(TREMBLREL. 07, LAST ANNOTATION UPDATE)
CEPTOR, SUBTYPE BETA.
                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AΑ;
                                                      CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHORDATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=PROSTATE;
K E., PELTO-HUIKKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S.A. 93:5925-5930(1996).
NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 3274;
Pred. No. 0.(
35; Mismatc)
                                                      VERTEBRATA;
                                                                                                                      PRT;
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                                                                                                                      485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11;
).00e+00;
ches 20;
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X
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                                                       TETRAPODA; MAMMALIA;
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Best Local S
Matches 42
                                                                                                                                                                                                                                                                                                                              035785;
035785;
01-JAN-1998
01-JAN-1998
01-JUN-1998
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PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
PFAM; PF00104; hormone_rec.
PFAM; PF00105; zf-C4.
RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING; ZINC-FINGER.
                                                                                                                                                                                                                                                                                                             01-JAN-1998 (TREMBLREL. (
01-JAN-1998 (TREMBLREL. (
01-JUN-1998 (TREMBLREL. (
0ESTROGEN RECEPTOR BETA2
ENDOCRINOLOGY 0:0-0(1998)
-!- SUBCELLULAR LOCATION:
EMBL; AJ002603; E1184907;
                                                     PETERSEN D.N.,
BROWN T.A.;
                                                                                                                                                                 STRAIN-WISTAR;
ALDRIDGE T.C.;
                                                                                                                                                                                                                                                          RATTUS NORVEGICUS (
EUKARYOTA; METAZOA;
                                                                                     STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                               SUBMITTED
                                                                                                                                                                                                                                                                                               ERBETA.
                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                          EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                526
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427; Conser
                                                                                                                                                                                                    FROM
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                                                                                                                                               (NOV-1997)
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                                                                                                                                                                                                                                                          (RAT).
A; CHORDATA;
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                  NUCLEAR
                                                                      .T.,
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Pred. No. 0.
36; Mismatc
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LAST SEQUENCE LAST ANNOTED
                                                                                                                                                                                                                                                           VERTEBRATA;
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                                                                       KOZA-TAYLOR
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ANNOTATION
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                  SIMILARITY)
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0.00e+00;
ches 22;
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                                                                       P.H.,
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Query
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01-AUG-1998 (TREMBLREL. 07, L
01-AUG-1998 (TREMBLREL. 07, L
ESTROGEN RECEPTOR BETA 2.
RATTUS NORVEGICUS (RAT).
EUKARYOTA: METAZOA; CHORDATA;
                                                            STRAIN-WISTAR: TISSUE-OVARY:
STRAIN-WISTAR: TISSUE-OVARY:
MARUYAMA K., ENDOH H., SASAKI-IWAOKA H., KANOU H.,
HASHIMOTO S., KATO S., KAWASHIMA H.;
BIOCHEM. BIOPHYS. RES. COMMUN. 246:142-147(1998).
BIOCHEM. BIOPHYS. RES. COMMUN. 246:142-147(1998).
                  RECEPTOR; TR
ZINC-FINGER.
SEQUENCE 5
                                                                                                                                                                                                    070195
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PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
PFAM; PF00104; hormone_rec.
PFAM; PF00105; zf-C4.
RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING;
                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                  EUTHERIA; RODENTIA.
                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                               PROSITE;
                                                                                                                                                                                                                                                     508
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 Match
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                                             SUBCELLULAR LOCATION: NUCLEAR (BY L; AB012721; D1026359; -. SITE; PS00031; NUCLEAR_RECEPTOR; 1.
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                                                                                                                                                                                                                                                                                                                                                                     YRIVRRORSSSEQVHCLSKAKRNGGHAPRVKELLLSTLSPEQLVLTLLEAEPPNVLVSRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.1%;
Similarity 85.9%;
                                     TRANSCRIPTION REGULATION;
                  503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             503 AA;
                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                   8
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                                                                                                                                           CHORDATA;
                   56216
78
                   ME.
                                                                                                                                                                       CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 3089; DB 11;
Pred. No. 0.00e+00;
34; Mismatches 19
Score
                                                                                                                                                                                                                                                                       503
                                                                                                                                                                                                              PRT;
                                                                                                                                            VERTEBRATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41300EB4 CRC32;
                  56067E12
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3076;
                                   1.
DNA-BINDING;
                                                                                                                                                                                                               503
                  CRC32;
                                                                                                                                                                                                              B
BB
                                                                                                                                           TETRAPODA;
11;
                                                                                                                                                                       UPDATE)
Length
                                     NUCLEAR
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                                                                                             SHIMAYA
                                                                                                                                            MAMMALIA;
503;
                                     PROTEIN;
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Matches
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                                                                                                                                                                                                  RECEPTOR; TR
ZINC-FINGER.
SEQUENCE 4
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-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)
EMBL; AF042060; G2801695; -.
PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING;
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01-JUN-1998 (TREMBLREL.
01-JUN-1998 (TREMBLREL.
ESTROGEN RECEPTOR BETAL
                                                                                                                                                                                                                                                                                                                                                            STRAIN-SPRAGUE-DAWLEY;
PETERSEN D.N., TKALCEVIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RATTUS NORVEGICUS (RAT)
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                                                        MTFYSPAVMNYSVPGSTSNLDGGPVRQSTSPNVLWPTSGHLSPLATHCQSSLLYAEPQKS
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YRLVRRQRSADEQLHCAGKAKRSGGHAPRVRELLLDALSPEQLVLTLLEAEPPHVLISRP
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PWCEARSLEHTLPVNRETLKRKLSGSSCASPVTSPNAKRDAHFCAVCSDYASG\(\frac{1}{2}\)HYGVWS 120
                                   MTFYSPAVMNYSIPSNVTNLEGGPGRQTTSPNVLWPTPGHLSPLVVHRQLSHLYAEPQKS 105
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393; Conser
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llarity 81.0%;
Conservative
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. 06, LAST SEQUENCE UPD
. 06, LAST ANNOTATION UPD DELTA3.
                                                                                                                                                                                                                                                                                                                                                              G.T.,
                                                                                                                Score 2545; DB 11;
Pred. No. 0.00e+00;
34; Mismatches 19
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-!- SUBCELLULAR LOCATION: NUCLEAR (BY EMBL; AF042061; G2801697; -...
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
RECEPTOR; TRANSCRIPTION REGULATION; DN ZINC-FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY;
PETERSEN D.N., TKALCEVIC
BROWN T.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESTROGEN RECEPTOR BETA2 ERBETA.
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01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UP
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION
ESTROGEN RECEPTOR BETA2 DELTA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RATTUS NORVEGICUS (RAT)
EUKARYOTA; METAZOA; CHC
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      142
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                                                                                                                              PWCEARSLEHTLPVNRETLKRKVSGNRCASPVTGPGSKRDAHFCAVCSDYASGYHYGVWS
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YRIVRRQRSSSEQVHCLSKAKRNGGHAPRVKELLLSTLSPEQLVLTLLEAEPPNVLVSRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CEGCKAFFKRSIQG---
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                                          CEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRERCG
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393; Conser
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larity 78.1%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                               MW;
                                                                                                                                                                                                                                                                                                       Score 2347; DB 11;
Pred. No. 0.00e+00;
34; Mismatches 19;
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013012;
01-JUL-1997 (TREMBLREL. 04, CREALL,
01-JUL-1997 (TREMBLREL. 07, LAST SEC
1 01-AUG-1998 (TREMBLREL. 07, LAST AND
E ESTROGEN RECEPTOR.
DANGUILLA JAPONICA (JAPANESE EEL).
S ANGUILLA JAPONICA (JAPANESE EEL).
C CSTEICHTHYES; ACTINOPTERYGII; ANGU
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 31
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TISSUE=LIVER;
TODO T.;
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013012
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PFAM; PF00105; zf-C4.
RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TODO T., ADACHI S., YAMAUCHI K.;

MOL. CELL. ENDOCRINOL. 119:37-45(1996).

-i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

EMBL; AB003356; D1020638; -.

PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZINC-FINGER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=LIVER;
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                         TNQCTIDKNRRKSCQACRLRKCYEVGMMKCGVRRERCTYRGARHRRMPHIRELAGTGGGA
                                                                                        SGNRCASPYTGP-GSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPA
                                                                                                                  ESEEGTSSVGGCFAGKGDMHFCAVCHDYASGYHYGVWSCEGCKAFFKRSIQGHNGYICPA
                                                                                                                                                                                                        SLSPSLFWPAHGHHGHVSPLALHFQQPLVYREPAHSPWAEPKPLEHGQAQTSKLAGKRMA 149 : | | : : : | | : : : : | | :
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                                                                                                                                                                                                                                                                                                                                                                  310;
                                                                                                                                                                                                                                                                                                                                                                                  h 57.4%;
Similarity 58.9%;
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04, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDATE)
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                                                                                                                                                                                                                                                                                                                                                               Score 2240; DB 13;
Pred. No. 0.00e+00;
101; Mismatches 98
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Best Local
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O91250;
O1-NOV-1996 (TREMBLREL. O1, CREATED)
O1-NOV-1996 (TREMBLREL. O6, LAST SEQUENCE UP
O1-JUN-1998 (TREMBLREL. O6, LAST ANNOTATION
ESTROGEN RECEPTOR.
POEPHILA GUTTATA (ZEBRA FINCH).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TE
                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00104; hormone_rec.
PFAM; PF00105; zf-C4.
RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-HYPOTHALAMUS-PREOPTIC AREA;
JACOBS E.C., ARNOLD A.P., CAMPAGNONI A.T.;
J. STEROID BIOCHEM. MOL. BIOL. 59:0-0(0).
-i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL; L79911; G1449146; -.
EMBL; L79911; G1449146; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                   YSSTTLSYAPTSESEG-SSSLAGFHS-LNSVPPSPVVFLQTAPHWSPFIHHHSQQVPYYL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CKNVVPVYDLLLEMLNAHVLRGCKSSIT-GSECSP-AEDSKSKEGS
                                                   GGIRKDRRGGRVMKQKRQREEQDSRNGEASSTELRAPTLWASPLVVKHNKKNSPALSLTA 304
                                                                                                                                                                                                                                                                  YPAMTF-YSPAVMNYSIPSNYTNLEGGPGRQTTSPNYLMPTPGHLSPLVVHR-QLSHLYA 100
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               HDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEIFDMLLATA 424
                                                                                                       CGSRRERCGYRLVRRQRSADEQLHCAGKAKRSGGHAPRVRE--LLL----D--ALS--P
                                                                                                                                                                        SGYHYGVWSCEGCKAFFKRSIQGHNDYMCPATNQCTIDKNRRKSCQACRLRKCYEVGMMK 244
                                                                                                                                                                                                               ENDOGSFGMREAAPPAFYRPNSDNRRHSIRERMSSANEKGSLSMESTKETRYCAVCNDYA 184
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                                                                                                                                                            SGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRKCYEVGMVK
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                                                                                                                                                                                                                                                                                                                                                                              66553 MW; 71DF4848 CRC32;
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LAST SEQUENCE UPDATE)
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RESULT 14
ID Q13511;
AC Q13511;
AC Q13511;
AC Q13511;
DT Q1-NOV-1996 (TREMBLREL. 01, C1)
DT Q1-NOV-1998 (TREMBLREL. 06, L1)
DT Q1-NOV-1998 (TREMBLREL. 06, L1)
DT Q1-JUN-1998 (TREMBLREL. 06, L1)
DE 80 KDA ESTROGEN RECEPTOR.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA;
CC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BREAST;
RX MEDLINE; 96174665.
RA NUCLEIC ACIDS RES. 24:962-969
CC -1- SUBCELLULAR LOCATION: NUCCEMBL; U47678; G1197855; -1-
DR PROSITE; PS00031; NUCLEBR_RC
DR PFAM; PF00104; hormone_Fec.
DR PFAM; PF00104; hormone_Fec.
DR PFAM; PF00105; Zf-C4.
KW RECEPTOR; TRANSCRIPTION REGUL
KW ZINC-FINGER.
SQ SEQUENCE 701 AA; 78430 MW;
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Best Local 9
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Q91424;
Q91424;
Q1-NOV-1996 (TREMBLREL. Q1, CREATED)
Q1-NOV-1996 (TREMBLREL. Q1, LAST SEQUE
Q1-JUN-1998 (TREMBLREL. Q6, LAST ANNOT
ESTROCEN RECEPTOR (FRACMENT).
CNEMIDOPHORUS UNIPARENS.
EUKARYOTA; ANIMALIA; METAZOA; CHORDATA
LEPIDOSAURIA; SQUAMATA.
                                                                                                                      Q91424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 96174665.

PINK J.J., WU S.Q., WOLF D.M., BILIMORIA M.M., JO NUCLEIC ACIDS RES. 24:962-969(1996).

-: SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY) EMBL; U47678; G1197855; -.

PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.

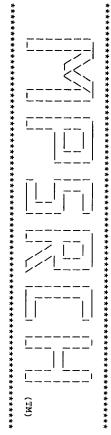
PFAM; PF00104; hormone_rec.

PFAM; PF00105; zf-C4.

RECEPTOR; TRANSCRIPTION REGULATION; DNA-BINDING;
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701 AA;
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l Similarity 56.9%;
197; Conservative
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Pred. No. 0.00e+00;
85; Mismatches 49
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       CHORDATA; VERTEBRATA; REPTILIA;
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                                                           SEQUENCE UP
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                                                                          UPDATE)
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                                                           UPDATE)
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Best Local Similarity 56.7%;
Matches 174; Conservative
                                           467
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                                                                                       HASNKGM 473
                     HMSNKGM 307
                            2 16:36:13 1998
                                                                                                       Score 1227; DB 13;
Pred. No. 1.08e-255;
68; Mismatches 53;
                                                                                                       Indels 12;
                                                                                                              Length 307;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Nov 2 16:36:30 1998; MasPar time 7.02 Seconds 534.685 Million cell updates/sec

Tabular output not generated.

Description: Perfect Score: Sequence: >US-08-906-365-2 (1-530) from US08906365.pep 3904 1 MDIKNSPSSLNSPSSYNCSQ......ECSPAEDSKSKEGSQNPQSQ 530

Scoring table: PAM 150 Gap 11

Searched: 77309 seqs, 7078906 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

Statistics:

a-issued 1:5_COMB 2:PCT9_COMB 3:backfiles1

Mean 33.550; Variance 151.595; scale 0.221

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ce 2,	Patent No. 5171671.	ati	,8	œ	8	2	Sequence 4, Applicatio	Patent No. 5223606.	Patent No. 5223606.	ъ	ζ,	6	2	2,	Sequence 4, Applicatio	4	4	2	Sequence 5, Applicatio	Patent No. 5223606.	Patent No. 5223606.	Patent No. 5223606.		Description
5.40e-2		09.	9.69e-	9.69€	9.69e-	1.86e-2	1.86e-	1.91e-2	91e	1.27e-2	1.11e-	1.11e-3	3.98e-3	3.98e-3	3.23e	ω	1.4	5	ر ح	.04e-4	1.47e-48	5.61e-141	1	Dred No

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ALIGNMENTS

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241 DMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITDT 300	181 GFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPVKLLFAPNLLLDRNQGKCVEGMVEIF 240 : : : : : : : : : : :: :: :: ::	121 SLALSLTADQMVSALLDAEPILYSEYDPTRPFSBASMMGLITNLADRELVHMINWAKRVP 180 :: :	61 CYEVGMMKGGIRKDRRGGRMLKHKRQRDDGEGRGEVGSAGDMRAANLWPSPLMIKRSKKN 120 :: :: :: : ::: : :: : ::	1 CAVCNDYASGYHYGVWSCEGCKAFFKRSIQGHNDYMCPAINQCTIDKNRRKSCQACRLRK 60 -	Ouery Match 42.2%; Score 1648; DB 3; Length 410; Best Local Similarity 56.9%; Pred. No. 5.61e-141; Matches 224; Conservative 92; Mismatches 64; Indels 14; Gaps 11;	. 5223606 5223606 5223606 5223606 CANT: BLAUDIN DE THE, HUGHES GLAN, ANNE OF INVENTION: STEROID/THYROI NAPPROPRIATELY EXPRESSED IN HR OF SEQUENCES: 11 R OF SEQUENCES: 11 R OPELICATION DATA: LICATION NUMBER: US/07/134,1 ING DATE: 17-DEC-1987 APPLICATION DATA: 15: 15: 15: 15: 16:H1: 410 444 AA; 50020 MW; 1110634 C	RESULT 1 ID 5223606-5 STANDARD: PRT: 444 AA.

Gaps

60

171

384 229 326 112 208

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RESULT 2
ID 5223606-6
XX
AC XXXXXX
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AC XXXXXX
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DT 01-JAN-1900
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DE Patent No.
CC Patent No.
CC Patent No.
CC PIERE: DEJ'C.
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ID 5223606-7
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                    Patent No. 5223
APPLICANT:
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         PIERRE; DEJEAN,
                                                             Patent No.
                                                                                       01-JAN-1900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYEVGMVKCGSRRERCGYRLVRRQRSADEQLHCAGKAKRSGGHAPRVRELLLDALSPEQL
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                                                                                                                                                                                             ISSQQQSMRLANLL-MLLSHVRH
                                                                                                                                                                                                                       VSSSQRFYQLTKLLDNLHDLVKQ
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CE 393 AA; 44638 MW; 907537 CN;
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Similarity 32.2%;
104; Conservative
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Pred. No. 1.47e-48;
88; Mismatches 120;
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                       HUGHES; MARCHIO, AGNES; TIOLLAIS
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Best Local Similarity
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SEQUENCE 386 AA:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                   SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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                                                CLASSIFICATION:
                                                             APPLICATION NUMBER: FILING DATE: 199106
                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 20036-5601
                                                                                                                                                                                                                       STREET:
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         REGISTRATION NUMBER:
                       NAME:
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                     Scott,
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Garabedian, M. J.
VENTION: SUPER GLUCOCORTICOID RECEPTORS
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                                                      UMBER: US/07/716,827C
19910619
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Pred. No. 7.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)8613000
TELEPAX: (202)822-8944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                          XXXXXX
                                                                                                                                                                                                                                                                   Sequence 2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 424 SPPSSSSAATGPPPKLCLYCSDEASGCHYGYLTCGSCKYFFKRAVEGQHNYLCAGRNDCI 483
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                                                                                                                                                                                                                                                Sequence 2, Application
                                                                                                                                                                                                                                       Patent No.
                                                               ZIP: 94105
COMPUTER READALE FORM:
MEDIUM TYPE Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
                                                                                                                                                                                                                              GENERAL INFORMATION:
       ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A
REGISTRATION NUMBER: 31,677
                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                 TITLE OF INVENTION: A NEW MEMBER OF THE NUCLEAR HORMONE TITLE OF INVENTION: RECEPTOR SUPERFAMILY AND A CDNA CLO
                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                           SLPCMYDQCKHMLFVSSELQRLQVSYEEYLCMKTLLLLSS 692
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                                                                                                                                         CITY:
STATE:
                                   APPLICATION NUMBER: U: FILING DATE: 19920928 CLASSIFICATION: 435
                                                                                                                                 COUNTRY:
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TYPE: AMINO ACID
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llarity 32.9%;
Conservative
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NUMBER:
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                                                       US/07/952,800
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Patent No. 1NFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein pence 533 AA; 56921 MW;
                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNQCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRERCGYRLVRRQRSADEQLHCAGKAKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VYDLLLEMLNA-HVL
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            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING YESTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                         COUNTRY: UZIP: 94105
                                                                                                                         STATE:
                                                                                                                                                      STREET:
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Similarity 34.1%;
                                                                                                                                                                                                                                                                              4, Application 
o. 5403925
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         Application US/07952800
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1 MARKET PLAZA,
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                                                                                                                                                                                                                                                                                          US/07952800
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Pred. No. 6.07e-37;
85; Mismatches 132
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                                                                                                                                                      TOWER,
               Version
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Query Match
Best Local S
Matches 12
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                                                                                                                                                                        Sequence 4, Application US/08336408E Patent No. 5723329
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SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
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                                                                                                                                                         GENERAL INFORMATION:
                        CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN &
STREET: 444 SOUTH FLOWER STREET, SUITE 2000
                                                                        TITLE OF INVENTION: RETINOI TITLE OF INVENTION: METHODS NUMBER OF SEQUENCES: 7
                                                                                                      APPLICANT: EVANS, RONALD M.
APPLICANT: MANGELSDORF, DAVID J.
TITLE OF INVENTION: RETINOID RECEPTOR COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
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NAME: Weber, Kenneth A
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                   VYDLLLEMLNA-HVL 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 19920 CLASSIFICATION: 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 AA; 48023 MW;
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llarity 34.1%;
Conservative
LOS ANGELES
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Pred. No. 1.40e-36;
84; Mismatches 133;
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Best Local Similarity
           Sequence 4, Application PC/TUS9100399
                                                                          XXXXXX
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                                                                                                         PCT-US91-00399-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PILING DATE: 22-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/478
FILING DATE: 09-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: RESITER, STEPHEN E.
REGISTRATION NUMBER: 91,192
REFERENCE/DOCKET NUMBER: P41
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT
FILING DATE: 22-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein ENCE 467 AA; 51216 MW; 1083042 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                                                                                                                      ISSQQQSMRLANLLMLLSHVRHASNKGMEHLLNMKCKNVVPVYDLLLEMLNA
                                                                                                                                                                                                  YP-EQPG-REAKLLLRLPALRSIGLKCLEHLFFFKLIGDTPIDTFLMEMLEA
                                                                                                                                                                                                                                                                  KMRDMQMDKTELGCLRAIVLFNPDSKGLSNPA-EVEA---L-R--EKVYASLE-AYCKHK 412
                                                                                                                                                                                                                                                                                                                                QVILLRAGWNELLIASFSHRSIAVKDGILLATGLHVHRNSAHSA-GVGAIFDRVLTELVS
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                                                                                                                                                                                                                                   RFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDADSSRKLAHLLNAVTDALVWVIAKSG
                                                                                                                                                                                                                                                                                                  QVRLLESCWMEVLMMGLMWRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFDMLLAT-TS
                                                                                                                                                                                                                                                                                                                                                                                              PKTETYVEANMG--L-N-PSSP-NDP--VTNICQAADKQLFTLVEWAKRIPHFSELPLDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: ami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
ZIP: 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 619-546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116;
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amino acid
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                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO PCT/US91/00399
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Pred. No. 3.23e-35;
89; Mismatches 119
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Length 467;

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RESULT

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TITLE OF INVENTION: APPLICANT: Mangelsdor APPLICANT: Evans Dr.,

NUMBER OF SEQUENCES:

STREET: 135 Sc CITY: Chicago ADDRESSEE:

Illinois

USA

60603

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138 HICAICGDRSSGKHYGYYSCEGCKGFFKRTVRKDLTYTCRDNKDCLIDKRQRNRCQYCRY 197
                                                                                                                                                                                                                                                                                                                                                                      147 HFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (619) 552-0095
TELEX: 20 6566 PATLAW CGO
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (619) 552-1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 07/4:
FILING DATE: 09-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Mr., Steph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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                                                                ISSQQQSMRLANLLMLLSHVRHASNKGMEHLLNMKCKNVVPVYDLLLEMLNA
                                                                                                                                                                                                                                                                 PKTETYVEANMG--L-N-PSSP-NDP--VTNICQAADKQLFTLVEWAKRIPHFSELPLDD
                                                                                                                                                                                                                                                                                                          RKCYEVGMVKCGSRRERCGYRLVRRQRSADEQLHCAGKAKRSGGHAPRVRELLLDALSPE
                                                                                                                                                                                                                                                                                                                                        QKCLAMGMKREAVQEER-Q-R-GK-DRNENE-VESTSSAN----EDMP-VEKILEAELAVE
                                                                                                                                                         KMRDMOMDKTELGCLRAIVLFNPDSKGLSNPA-EVEA---L-R--EKVYASLE-AYCKHK
                                                                                                                                                                                       QVRLLESCWMEVLMMGLMWRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFDMLLAT-TS
                                                                                                                                                                                                                                                 QLVLTLLEAEPPHVLISRPSAPFTEASMMMSLTKLADKELVHMISWAKKIPGFVELSLFD
                                                                                             YP-EQPG-RFAKLLLRLPALRSIGLKCLEHLFFFKLIGDTPIDTFLMEMLEA 462
                                                                                                                           RFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDADSSRKLAHLLNAVTDALVWVIAKSG
                                                                                                                                                                                                                   QVILLRAGWNELLIASFSHRSIAVKDGILLATGLHVHRNSAHSA-GVGAIFDRVLTELVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Reiter, Mr., Stephen REGISTRATION NUMBER: 31192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: POFILING DATE: 19910122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LE TYPE: protein
467 AA; 51216 MW; 1083042 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       467 amino acids
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      STANDARD;
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Pred. No. 3.23e-35;
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TOPOLOGY: inear
MOLECULE TYPE: protein
MOLECULE TYPE: 50811 MW; 1063517 CN;
TOPOLOGY: 462 AA; 50811 MW; 20010 513; D.

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APPLICANT: EVANS,
APPLICANT: MANGEL:
                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: WO PCI
FILING DATE: 22-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07,
FILING DATE: 09-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 08-NOV-19-
CLASSIFICATION: 435
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APPLICATION NUMBER: 1
FILING DATE: 21-AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 21-AUG-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                 QVILLRAGWNELLIASFSHRSIAVKDGILLATGLHVHRNSAHSA-GVGAIFDRVLTELVS
                                             QLVLTLLEAEPPHVLISRPSAPFTEASMMSLTKLADKELVHMISWAKKIPGFVELSLFD
                                                                          PKTETYVEANMG--L-N-PSSP-NDP--VTNICQAADKQLFTLVEWAKRIPHFSELPLDD 296
                                                                                                         RKCYEVGMVKCGSRRERCGYRLVRRQRSADEQLHCAGKAKRSGGHAPRVRELLLDALSPE
                                                                                                                                       QKCLAMGMKREAVQEER-Q-R-GK-DRNENE-VESTSSAN---EDMPVER-ILEAELAVE 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: Patentl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & STREET: 444 SOUTH FLOWER STREET, SUITE 2000 CITY: LOS ANGELES
STATE: CA
                                                                                                                                                                                                                                116;
                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                           h 13.1%;
Similarity 33.0%;
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WENTION: RETINOID RECEPTOR COMPOSITIONS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn Release #1.0, Version
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 3.98e-35;
89; Mismatches 119
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Matches Query Match

Local Similarity 33.0%; mes 116; Conservative

13.28;

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SEQUENCE

MOLECULE TYPE:

TYPE: AMI

AMINO ACID

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386 361 327 302 267 249

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Query Match
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                                             133 HICAICGDRSSGKHYGVYSCEGCKGFFKRTVRKDLTYTCRDNKDCLIDKRQRNRCQYCRY 192
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                                                                                                                                                              TELEFAX: (619) 552-0095
TELEX: 20 6566 PATLAW CGO
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acid
TYPE: AMINO ACID
TYPE: AMINO ACID
                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/478,071
FILING DATE: 09-FEB-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/0039 FILING DATE: 19910122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 552-1311
                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Mangelsdorf, Dr., APPLICANT: Evans Dr., Ronald
                 QKCLAMGMKREAVQEER-Q-R-GK-DRNENE-VESTSSAN---EDMPVER-ILEAELAVE 243
                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: RETINOID RECEPTOR COMPOSITIONS AND TITLE OF INVENTION: METHODS
 RKCYEVGMVKCGSRRERCGYRLVRRQRSADEQLHCAGKAKRSGGHAPRVRELLLDALSPE
                                   HFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRL
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                                                                                                                                                                                                          NAME: Reiter, Mr., Stephen E. REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: 5085
                                                                        116;
                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                     STREET: 135 Sout
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                            NAME:
                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                          462 AA;
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FITCH, EVEN, TABIN & FLANNERY
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50811 MW; 1063517 CN;
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33.0%;
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Pred. No. 3.98e-35;
89; Mismatches 119;
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GENERAL INFORMATION:
APPLICANT: EVANS, RONALD M.
APPLICANT: MANGELSDORF, DAVID
APPLICANT: MANGELSDORF, DAVID
APPLICANT: MANGELSDORF, DAVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   446 ISSQQQSMRLANLLMLLSHVRHASNKGMEHLLNMKCKNVVPVYDLLLEMLNA 497
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                                                                                                                                                               TELEPHONE: 619-546-19
TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: WO POST FILING DATE: 22-JAN-1991 PRIOR APPLICATION DATA: APPLICATION NUMBER: US OF APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 619-546-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 09-FEB-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                               NAME: REITER, STEPHEN E REGISTRATION NUMBER: 31
                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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444 SOUTH FLOWER STREET,
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LOWER STREET, SUITE 2000
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Best Local S
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                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, v
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/00399
FILING DATE: 19910122
CLASSIFICATION DATA:
APPLICATION UMBER: 07/478,071
FRILING DATE: 09-FEB-1990
                                                                                                                                                                                                                                                                                                   Sequence 6, Application PC/TUS9100399
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nes 117; Conservative
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            ATTORNEY/AGENT INFORMATION:
Steph
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                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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                                                                                                                                                                                CITY: Chicago
STATE: Illinois
REGISTRATION NUMBER:
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          Reiter,
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        Mr., Stephen
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                                                                                                     Release #1.0, Version
                                                                                PCT/US91/00399
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Pred. No. 1.11e-32;
94; Mismatches 120;
                                                                                                                                                                                                                                                                             David J.
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Best Local Similarity 32.2%;
                                                                                                                                                         APPLICANT: TAKAKU, FUMIMARO;ISI
EVANS, RONALD M.;UMESONO, KAZUHIKO
TITLE OF INVENTION: HUMAN GAMMI
NUMBER OF SEQUENCES: 4
                                                                                                            SEQ ID NO:
                                                                                     SEQUENCE
                                                                                                                                                                                                         Patent No. 5260432
                                                                                                                                                                                                                                  Patent No.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-1311
TELEFAX: (619) 552-095
TELEX: 20 6566 PATLAW CGO
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
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                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/370,407
FILING DATE: 22-JUN-1989
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MOLECULE TYPE: protein
JENCE 463 AA; 50978 MW; 1097932 CN;
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                                                                                    LENGTH: 454
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99; Conse
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                                      11.3%;
larity 28.4%;
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                                                                                     54527 MW; 1333563 CN;
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                                     Score 441; DB 3;
Pred. No. 1.27e-28;
88; Mismatches 140
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Pred. No. 1.11e-32,
94; Mismatches 120
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APPLICANT: BLAUDIN DE THE, HUGHES; MARCHIO, AGNES; TIOLLAIS, PIERRE; DEJEAN, ANNE
TITLE OF INVENTION: STEROID/THYROID HORMONE RECEPTOR-RELATED PROTEIN INAPPROPRIATELY EXPRESSED IN HUMAN HEPATOCELLULAR CARCINOMA NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 368
SEQUENCE 398 AA; 44842 MW; 907111 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ
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Local Similarity 26.9%;
les 94; Conservative
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                                                                                  TLLKAAC-LDILILRICTRYTPEQDTMTFSDGLTLNRTQ-MHNAGFGPLTDLVFTFANQL 229
                                                                                                                                                                                                                                                                                                                                       CAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCTIDKNRRKSCQACRLRK 208
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                                                                  RELKLQHKEYLCVKAMILLNSSMYPLVTATQDADSSRKLAHLLNAVTDALVWVIAKSGIS
                                                                                                                                     RLL-ESCWMEVLMMGLMWRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFDMLLATTSRF
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                               SKPH-M-FPKILMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMME
SQQQSMRLANLLMLLSHVRHASNKGMEHLLNMKCKNVVPVYDLLLEMLN
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Pred. No. 1.91e-28;
97; Mismatches 136;
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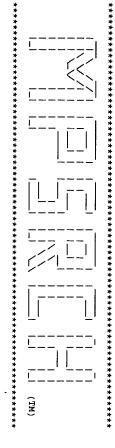
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Best Local Similarity 26.9%;
Matches 94; Conservative
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APPLICANT: BLAUDIN DE T
PIERRE; DEJEAN, ANNE
TITLE OF INVENTION: STER
PROTEIN INAPPROPRIATELY EXPR
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CURRENT APPLICATION DATA:
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FILING DATE: 17-DEC-1987
PRIOR APPLICATION DATA:
                                                                                                                                         TLLKAAC-LDILILRICTRYTPEQDTMTFSDGLTLNRTQ-MHNAGFGPLTDLVFTFANQL 309
                                                                                                                                                                       VLTLLEAEPPHYLISRPSAPFTEASMMSLTKLADKELVHMISWAKKIPGFVELSLFDQV
                            SKPH-M-EPKILMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMME
                                                                       LPLEMDDTE----TG--LL-SAICLICGDRQDLEEPTKVDKLQEPLLEALK-IYIRKRRP 361
                                                                                                                RLL-ESCWMEVLMMGLMWRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFDMLLATTSRF
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                                                         RELKLQHKEYLCVKAMILLNSSMYPLVTATQDADSSRKLAHLLNAVTDALVWVIAKSGIS
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                                                                                                                                                                                                                                                                                                                                                                                                  485 AA; 54437 MW; 1345912 CN
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Pred. No. 1.91e-28;
97; Mismatches 136;
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Search completed: Mon Job time: 44 secs. Nov N 16:37:14 1998

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MPsrch_nn n.a. n.a. database search, using Smith-Waterman algorithm

Run on: Tue Nov 3 04:15:30 1998; MasPar time 2128.26 Seconds 1215.488 Million cell updates/sec

Tabular output not generated.

Title:

>US-08-906-365-1 (1-1686) from US08906365.seq 1686

Description:
Perfect Score:
N.A. Sequence:
Comp: 1 cagccattatacttgcccac......agaacccacagtctcagtga 1686 gtcggtaatatgaacgggtg......tcttgggtgtcagagtcact

Scoring table: TABLE default Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 1988617 segs, 767163441 bases × 2

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: Database: 1:em_est10 2:em_est11 genbank-est107

embl-est55

3:gb_est1 4:gb_est10 5:gb_est11 6:gb_est12 7:gb_est13 8:gb_est14 9:gb_est15 10:gb_est16 11:gb_est17 12:gb_est18 13:gb_est15 10:gb_est2 15:gb_est20 16:gb_est21 17:gb_est22 18:gb_est23 19:gb_est24 20:gb_est3 21:gb_est4 22:gb_est5 23:gb_est6 24:gb_est7 25:gb_est8 26:gb_est9 27:gb_gss

Statistics: Mean 11.528; Variance 1.960; scale 5.882

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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16	21	21	10	13	16	16	7	13	13	13	15	BB
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legans cDNA clone 4a08.rl Soares pr 2d01.rl Soares mc 0g08.yl Sugano mc 0 sapiens ntcon2	8b11.r1 Strat o sapiens ntc 5a11.r1 Homo	WOS/T05.rl Soares mous MBAFCW4807T3 Brugia ma zv63a08.rl Soares tota zw47c03.rl Soares tota C.elegans cDNA clone y EST59103 Infant brain ETMR5917 HSC177 Celle	Homo sa Soares Activated Normaliz Soares	4739.5p1 3h03.s1 5d07.r1 0b06.r1	44a02.rl Stratagene 56a06.rl Soares mou 80b08.rl Soares mou 45e08.xl Soares_tes
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ALIGNMENTS

FEATURES source	TITLE JOURNAL COMMENT	ORGANISM REFERENCE AUTHORS	RESULT 1 LOCUS DEFINITION ACCESSION NID KEYWORDS SOURCE
Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: estewatson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1309 Std Error: 0.00 Seq primer: -28m13 rev1 ET from Amersham High quality sequence stop: 357. Location/Qualifiers 1. 531 /organism="Homo sapiens" /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: 0ligo dT. Differentiated, post mitotic hNT neurons. Average insert size: 1.5 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'	Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project Unpublished (1997)	Homo sapiens Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 531) Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,	AA224131 531 bp mRNA EST 11-MAR-1998 zr14e02.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone 648794 5', mRNA sequence. AA224131 g1844690 EST. buman.

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA744644 466 bp mRNA EST 07-FEB-1998 ny79f02.sl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1284507 similar to gb:M12674 ESTROGEN RECEPTOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                     High
                                                                                                                                                                                                                                                                                                                                                                                                                      Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D.,
Ph.D., Gerald Marti, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                             www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                        cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                numan.
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Sonaldo, Ph.D.
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             GAATTCGGCACGAG 3' -3' adaptor sequence:
CTCGAGTTTTTTTTTTTTTTT 3'"
/db_xxef="GDB:5589314"
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/clone="648794"
/clone_lib="Stratagene hNT neuron (#93:/dev_stage="hNT neurons"
/dev_stage="hNT neurons"
/lab_host="SOLR (kanamycin resistant)"
/lab_host="12 g 146 t 7 othe
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Pred. No. 0.00e+00;
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Query Match 4.0%;
Best Local Similarity 11.8%;
Matches 27; Conservative
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Best Local Similarity 82.8%;
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EST.
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97SN1787 Rice Immature Seed Lambda
cDNA clone 97SN1787, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                     Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of
University, Yongin, Korea. 449-728
Seq primer: M13 Reverse Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 252)
1 (bases 1 to 252)
Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Cytogenetics
National Inst. of Agri. Sci. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Eun M.Y.
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Lee,M.C. and Eun,M.Y.
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Embryophyta; Tracheophyta;
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                                                                                                                                                                                                                               /organism="Oryza sativa"
/Cultivar="Milyang23"
/Cultivar="Milyang23"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
/note="Vector: Directional cDNA library inserted into lambda ZAPI
XhoI; Directional cDNA library inserted into lambda ZAPI
Yector at 5'end with EcoRI and 3' end with Xho I site."
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                                                                                              /tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
21 c 12 g 35 t 179 ot
                                                                                                                                                                                              /clone="97SN1787"
                                                                                                                                                                                                                 /db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                          /clone_lib="Rice Immature Seed
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Score 68; DB 13;
Pred. No. 4.00e-88
123; Mismatches 7
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2.42e-105;
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bhnahm@bioserver.myongji.ac.kr
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VNWBNVSGDWHYWBVBNTKVDVGNHTRCSRWRBVTRM-AHYHDYTNCBBYNNNDYHMWHB 126
                               cgccccatgtgctgatcagccgccccagtgcgcccttcaccgaggcctccatgatgatgt 982
                                                     VRGCCCCBAWMITSYBCHGNBVWVCVASHGNYMSVHNCTBRGTHCDCKNVNWS-TMTWGT 67
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EST.
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Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.
Seq primer: M13 Reverse Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Cytogenetics
National Inst. of Agri. Sci.
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
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Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., F
Lee,M.C. and Eun,M.Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Eun M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Embryophyta; Tracheophyta;
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                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                   /note-"Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; Directional cDNA library inserted into lambda ZAPII vector at 5'end with EcoRI and 3' end with Xho I site." /db_xref="taxon:4530" /clone-"97SN1787"
                                                                                                                                                                                            /tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
21 c 12 g 35 t 179 ot
                                                                                                                                                                                                                                                                  /clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
                                                                                                                                                                                                                                                                                                                                                                           /cultivar="Milyang23"
                                                                                                                                                                                                                                                                                                                                                                                               /organism="Oryza sativa"
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                                                                                                                          3.7%;
14.2%;
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WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dub
Geisel, S., Kucaba, T., Lacy, M., Le, M., Marrin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA517920 534 bp mRNA EST vh95e10.rl Barstead mouse myotubes MPLRB5 Mus 902058 5' similar to gb:M34476 Mouse retinoic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
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3.6%;
llarity 66.7%;
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/db_xref="taxon:10090"
/clone="902058"
                                                                                                                                                                                                                                                                                                                                                                  3'); double-stranded cDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector.
                                                                                                                                                     /clone_lib="Barstead
/cell_line="C2C12"
                                                                                                                                                                                                                                                                Library constructed by Bob Barstead. The C2C12 cell line (available from ATCC, catalog # CRL-1772) differentiates
                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="C3H"
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atcgctgcagacagcgcaga
                                                         tttaaaaaaggccttacatccttcacacgaccagactccatagtgatatcccgatgcgta
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Fax: (301)-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Lee,
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1 (chases 1 to 384)
Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quacken Rerlavage, A.R. and Adams, M.D.
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primer: M13-21.
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larity 64.0%;
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/note="Organ: placenta; Vector: pT7T3Pac;
Site_2: Not1"
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102 c 94 g
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/clone="RPLAC64"
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Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.
   rice.
Oryza sativa
Cryza sativa
Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; L
                                                                       AA754458 247 bp mRNA EST 20-J
97SN1784 Rice Immature Seed Lambda ZAPII cDNA Library
cDNA clone 97SN1784, mRNA sequence.
AA754458
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EST.
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128; Conser
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clone RPLAF19 3' end,
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1 (bases 1 to 384)

Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.

Kerlavage,A.R. and Adams,M.D.
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/db_xref="taxon:10118"
/clone="RPLAF19"
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/note="Organ: placenta; Vector: pT7T3Pac;
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Pred. No. 4.37e-63;
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N. Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morr
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                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
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National Inst. of Agri. Sci.
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                                                                                                   house mouse.
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Similarity 14.8%;
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/cultivar="Milyang23"
/cultivar="Milyang23"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPI
vector at 5'end with EcoRI and 3' end with Xho I site."
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/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
16 c 21 g 34 t 169 ot)
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/clone="97SN1784"
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                   Dietrich, N.,
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                                                                 Eutheria;
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(ho I site."
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561

tgcgtaatcgctgcagacagcgca AGCGTTGTCGCCGCACACGGCACA 283

538

10

H91890 403 bp mRNA EST ys81d07.r1 Homo sapiens cDNA clone 221197 5 gb:X51417_cds1 STEROID HORMONE RECEPTOR ERR

ERR2

5,

29-NOV-1995 similar to (HUMAN);

gb:X51417_cds1 H91890

EST

g1087468

CDNA

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ORIGIN
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                                                                                                                                        CTTAACCATCCCGACACTGAGACACTTCTGAAATCTGCAGTACTGACATCCGGTTTCGGCG 139
gcttcttttaaaaaaggccttacatccttcacacgaccagactccatagtgatatcccga
                              CGTTCTCTTGAAGAAGCCCTTGCAGCCCTCGCAGGTGCGGACTCCGTAGTGCTGGCAGGC 259
                                                            gtttttatcgattgtacactgatttgtagctggacaaatataatcattatgtccttgaat
                                                                                                                        cttcaccattcccacttcgtaacacttccgaagtcggcaggcctggcagctcttgcgccg
                                                                                                                                                                                         128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
This clone is available royalty-free
IMAGE Consortium (info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop:
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Similarity 62.7%;
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                 Dr. Minoru Ko (Wayne State University)."
/db_xref="taxon:10090"
/clone="317263"
                                                                                                                                                                                                                                                                 /clone_lib="Soares mouse p3NMF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH1OB (ampicillin resistant)"
106 c 114 g 100 t
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                                                                                                                                                                                                      Score 52;
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Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteic Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; The Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 403)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
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                                                                                                                                                                                                                                   ys69h11.r1 Homo sapiens
gb:X51417_cds1 STEROID H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Location/Qualifiers
                                                                                                                                                                                           g1060631
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
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larity 66.7%;
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/clone="221197"
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LOCUS

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Allen, M.,

Bowles, L.,

Dubuque, T.,

Geisel, G.,

Jost,S.,

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REFERENCE
AUTHORS
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similar to
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Fax: 314 286 1810
Hillier, L.,
                                                         Eukaryotae;
Vertebrata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson
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/clone="220101"
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Soares NhHMPu S1 Homo sapiens cDNA clone 754804 5'
gb:m29960 STEROID RECEPTOR TR2 (HUMAN);, mRNA sequence
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EST.
                                                                                                         AA876157 280 bp mkNA px21b07.s1 NCI_CGAP_GC3 HOMO sapiens cDNA clone IMAGE:1256725 3' nx21b07.s1 hCI_CGAP_GC3 HOMO Sapiens cDNA clone IMAGE:1256725 3' similar to gb:M11050 GLUCOCORTICOID RECEPTOR, BETA (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 334.
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Fax: 314 286 1810
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Homo sapiens
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/note="Organ: mixed (see below); Vector: pT773D-Pac
/note="Organ: mixed (see below); Vector: pT773D-Pac
/(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260332-265223,
340488-345479, and 484488-489479."
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61.9%;
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                                                                                                                                                                                                                                             (HUMAN);, mRNA sequence.
AA157597
g1729205
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; H 1 (bases 1 to 412)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M
                                                                                                                                             human.
Homo sapiens
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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4444 Forest Park Parkway, Box 8501,
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                                              1 (bases 1 to 508)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                   W53545 508 bp mRNA EST 03-JUN-1996 md56a06.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 372370 5' similar to gb:x57528 M.musculus mRNA for retind acid receptor-alpha (MOUSE); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
WashU-Merck EST Project
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                                                                                                                                                         Eukaryotae; mitochondrial eukaryotes; Metazoa;
Vertebrata; Eutheria; Rodentia; Sciurognathi; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800 Fax: 314 286 1810
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              The WashU-HHMI Mouse EST Project
                                    Waterston, R.
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llarity 64.9%;
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/clone="589706"
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/lab_host="SOLR (kanamycin resistant)"
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                                                                                                                                                                         GCATCCAGAAGAACATGGTGTATACGTGTCACCGGGACAAGAACTGCATCATCAACAAGG 352
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                                                                          accggcgcaagagctgccaggcctgccgacttcggaagtgttacgaagtgggaatg
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    Location/Qualifiers
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Fax: 314 286 1810
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WashbrythmI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
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                                                                                                                                                                                                                                                                                                h 2.8%;
Similarity 63.6%;
112; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 ], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ, from 2 ], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatina Bonaldo."

/db xref="arxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Soares mouse
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Nov 2 16:24:20 1998; MasPar time 20.72 Seconds 413.984 Million cell updates/sec

Tabular output not generated.

Title:

Description: Perfect Score: >US-08-906-365-2 (1-530) from US08906365.pep 3904 1 MDIKNSPSSLNSPSSYNCSO... MDIKNSPSSLNSPSSYNCSQ......ECSPAEDSKSKEGSQNPQSQ 530

Scoring table: PAM 150 Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq32
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 36.033; Variance 154.129; scale 0.234

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result	Score	Query Match	Length	DB	ID	Description	Pred. No.
_	3904	100.0	530	28	W33215	Human oestrogen recep	0.00e+00
N	3582	91.8	485	21	W14724	oestrogen	0.00e+00
w	3532	90.5	477	28	W33212	oestrogen	0.00e+00
4	3274	83.9	485	21	W14723	estrogen re	0.00e+00
ហ	3250	83.2	485	21	W14725	Mouse oestrogen recep	0.00e+00
O	3099	79.4	416	27	W33213		4.32e-293
7	3099	79.4	418	28	W33214		4.32e-293
00	1714	43.9	233	27	W33211		2.24e-154
9	1671	42.8	595	N	P70543		4.30e-150
10	1424	36.5	334	N	P80925		1.58e-125
11	807	20.7	433	Ν	P80931	huma	1.04e-64
12	800	20.5	521	N	P80930	human	5.02e-64
13	614	15.7	777	N	P80919	н	5.47e-46
14	614	15.7	777	28	W44700	Mutant nuclear glucoc	5.47e-46
15	590	15.1	1070	23	W17789	Green fluorescent pro	1.11e-43
16	576	14.8	902	ω	R12224	Rat androgen receptor	2.46e-42
17	570	14.6	902	_	P93110	Rat androgen receptor	9.28e-42
18	570	14.6	902	μ	P91006		9.28e-42

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Zebrafish retinoid X	Mouse retinoic acid r	Skin-specific murine	oic acid	clear	Human retinoid X rece	Mouse RXR-gamma retin	gamma.	RXR-alpha	Mouse RXR-alpha retin	mRXR-alpha.	Sequence of the human	mRXR-beta.			H2RIIBP nuclear hormo	Human H-2RIIBP.	hRXR-beta1.	ຜ	Human oestrogen recep	/androgen rece	ogen re	∷ -	recep	Human androgen recept	₼	Human androgen recept
.77e-	.09e-	.49e-	3.09e-3	.57e-3	.66e-3	.69e-3	.03e-3	.29e-3	.10e-3	.10e-3	.52e-	.88e-3	.70e-3	.79e-3	.79e-3	.23e-3	.23e-3	.67e-3	.08e-3	.30e-3	.85e-3	.35e-4	.24e-4	.80e-	.80e-	9.28e-42

ALIGNMENTS

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Query Match 100.0%; Best Local Similarity 100.0%; Matches 530; Conservative	W33215 stan w33215; w3
100.0%; 100.0%; rvative	(first entry) ogen receptor protein; riol; screening. 2. 2. 2. 2. 2. 2. 2. 3. EP-203284. EP-203284. EP-200820. ONOBEL NV. NOSEL NV. Vosselman S; 188/44. 415. 198/44. 15. 198/45. 198/44. 15. 198/44. 15. 198/44. 15. 198/44. 15. 198/44. 15. 198/44. 15. 198/44. 15. 198/44. 10. 10. 10. 10. 10. 10. 10. 10. 10. 10
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                        Query Match
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08-SEP-1995; GB-018272.
15-MAR-1996; GB-005550.
11-APR-1996; GB-007532.
08-MAY-1996; GB-009576.
(KARO-) KARO BIO AB.
                                                                                                                                                                                                                                                                     WO9709348-A2.
13-MAR-1997;
09-SEP-1995;
08-SEP-1995;
15-MAR-1996;
11-APR-1996;
08-MAY-1996;
                                           Claim 1; Fig 13A; 45pp; English.

A novel human orphan receptor (W14724) is related to the known oestrogen receptor ER-alpha, and has been designated ER-beta. It is an oestrogen receptor-related nuclear receptor. The ER-bēta amino acid sequence was deduced from a CDNA clone (T62843) isolated from a human testis CDNA library. Rat, human and mouse ER-beta (W14723-25) can be used to isolate molecules for use in the treatment of cardiovascular diseases, central nervous system diseases, osteoporosis, prostate or ovarian cancer or benign prostatic hyperplasia and to test environmental chemicals for oestrogenic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human oestrogen receptor beta (ER-beta).
Orphan receptor; oestrogen receptor beta; ER-beta;
nuclear receptor; prostate cancer; benta prostatic
ovary cancer; cardiovascular disease; osteoporosis;
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  Conservative
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260..457
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    used to develop prods. for osteoporosis or cardiovascular

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01-OCT-1997.
25-MAR-1997; 2
22-NOV-1996; E
26-MAR-1996; E
                                                                                                                                                                    N-PSDB; T88412.

DNA encoding estrogen receptor - useful in screening assay to identify novel ligands or hormonal analogues Claim 4; Page 18-20; 45pp; English.

This sequence represents a novel oestrogen binding protein. The cD sequence which encodes this protein can be alternatively spliced resulting in the detection of additional transcripts (see T88413). This receptor is able to bind and be activated by estradiol, eston estriol, can be used in a screening assay for the identification o drugs e.g. novel ligands or hormonal analogues.

Sequence 477 AA;
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13-MAR-1997.
09-SEP-1996; E03933.
08-SEP-1996; GB-018272.
15-MAR-1996; GB-005550.
11-APR-1996; GB-007532.
08-MAY-1996; GB-009576.
(KARO-) KARO BIO AB.
Enmark E, Gustafsson J,
WPI; 97-192842/17.
                                                       Claim 1; Fig 1; 45pp; English.

A novel rat orphan receptor (W14723) is related to the known oestrogen receptor Er-alpha, and has been designated ER-beta. It is an oestrogen receptor related nuclear receptor. The ER-be amino acid sequence was deduced from a cDNA clone (T62842) isola from a rat prostate cDNA library. Rat, human and mouse ER-beta (W14723-25) can be used to isolate molecules for use in the treatment of cardiovascular diseases, central nervous system diseases, osteoporosis, prostate or ovarian cancer or benign prostatic hyperplasia and to test environmental chemicals for
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08-SEP-1995; GB-018272.

15-MAR-1996; GB-005550.

11-APR-1996; GB-007532.

08-MAY-1996; GB-009576.

(KARO-) KARO BIO AB.
                                                                                                                                        Enmark E, Gustafsson J,
WPI; 97-192842/17.
N-PSDB; T62844.
New isolated oestrogen r
                                                                                    disease
Claim 1;
A novel mouse orphan receptor (W14725) is related to oestrogen receptor ER-alpha, and has been designated It is an oestrogen receptor related nuclear receptor amino acid sequence was deduced from a course
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W14725;
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08-JUN-1997 (first entry)
Mouse oestrogen receptor beta (ER-beta).
Orphan receptor; oestrogen receptor beta; ER-beta;
nuclear receptor; prostate cancer; benign prostatic
                                                                                                                                                                                                                                                                                                                                                    WO9709348-A2.
13-MAR-1997.
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Best Local :
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                                                                                    EP-798378-A2.
01-OCT-1997.
25-MAR-1996; EP-203284.
26-MAR-1996; EP-203284.
26-MAR-1996; EP-200820.
(ALKU ) AKZO NOBEL NV.
Dijkema R, Mosselman S;
WPI; 97-473188/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            central nervous system diseases, osteoporosis, prostate or ovari cancer or benign prostatic hyperplasia and to test environmental chemicals for oestrogenic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           molecules for use
                                               DNA encoding estrogen receptor - us identify novel ligands or hormonal Claim 4; page 20-22; 45pp; English.
                                                                                                                                                                      Homo
         This partial sequence represents a splice variant of a novel cestribinding protein, detected by screening a human testis cDNA library This protein contains an alternative exon 8 (exon 8B) of the novel cestrogen receptor represented. As a consequence of the introduction
                                                                                                                                                                                       0estrogen
                                                                             N-PSDB; T88413
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                                                                                                    DNA encoding estrogen receptor - useful in screening assay to identify novel ligands or hormonal analogues Claim 4; Page 30-32; 45pp; English.

This sequence represents a splice variant of a novel oestrogen binding protein isolated from human thymus tissue. This protein contains an alternative exon 8 (exon 8C) of the novel oestrogen receptor represented in T88412. This novel receptor is able to bind and be activated by estradiol, estone and estriol, can be used in a screening assay for the identification of new drugs e.g. novel ligands or hormonal analogues.
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Sequence 418 AA;
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Dijkema R, Mosselman S;
WPI; 97-473188/44.
N-PSDB; T88412.
                                                                                                                                                                                                                                                                                                                          DNA encoding estrogen receptor - useful in screening assay to identify novel ligands or hormonal analogues Claim 4: Page 16-17; 45pp; English.

This sequence encodes the ligand binding domain of a novel constrogen binding protein, detected by screening a human testis cDNA library. This receptor is able to bind and be activated by estradiol, estone and estriol, can be used in a screening assay identification of new drugs e.g. novel ligands or hormonal
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Similarity 100.0%;
415; Conservative
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                                                                                                                                                                                        Score 1714; DB 27;
Pred. No. 2.24e-154;
0; Mismatches 1;
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No. 4.32e-293;
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Best Local 9
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WO8705049-A.

27-AUG-1987.

18-FEB-1987; U00341.

20-FEB-1986; US-833829.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig. 1-1 - 1-2; 26pp; English.

Disclosure; Fig. 1-1 - 1-2; 26pp; English.

Steroid receptor protein;

The protein is expressed in an expression system from cDNA operably

linked to control sequences compatible with eukaryotic host cells.

This method allows expression under conditions which favour appropriate
post-translational processing. It also produces large amts. of purified
protein useful in the design of agonist and antagonist cpds. for study
of the mechanism of action of the steroid binding proteins in general,
and for use in diagnostic assays for the proteins or antibodies to
them. These assays are important in, eg the diagnosis of tumour
sensitivities to steroid metabolism. Suitable host cells are VERO,

Hela and CHO cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CALB-) California Shine J;
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llarity 56.3%;
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Pred. No. 4.30e-150;
98; Mismatches 61;
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Best Local S
Matches 19
                                                                                                                                                                 05-MAY-1988.
23-OCT-1987; UU2782.
20-OCT-1987; US-108471.
(SALK) Salk Inst for Biol S
Evans RM, Weinberger CA, Ho
WPI; 88-133242/19.
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20-OCT-1987; US-108471.
(SALK) Salk Inst for Biol
Evans RM, Weinberger CA, H
WPI; 88-133242/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comprising glucocorticoid, mineral and novel hormone receptors Example; Fig III-2; 243pp; English
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Sequence of the human oestrogen
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P80931;
                                                                                   Recombinant DNA encoding
                                                                                                                                      N-PSDB; N80922
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DNAs encoding hormone receptors and the hormone receptors themselves are claimed. The DNA can be used to make the hormone receptor proteins and functional modified forms in quantities not previously possible. The receptor proteins can be used to screen cpds. for receptor-agonist or receptor-antagonist activity. They can also be used in diagnostic assays. Also claimed is pure DNA encoding oestrogen-related receptors hERR1 and hERR2 and hERR2 and hERR2. The new hERR1 and hERR2 receptors will provide
                                                                                                          comprising gluccocriticald, mineralocorticald, thyroid hormone and novel hormone receptors

Claim 17; Fig V-1(B)-1 and -2; 243pp; English.

DNAs encoding hormone receptors and the hormone receptors themselves claimed. The DNA can be used to make the hormone receptor proteins an functional modified forms in quantities not previously possible. The receptor proteins can be used to screen opds. for receptor-agonist or receptor-antagonist activity. They can also be used in diagnostic ass also claimed is pure DNA encoding oestrogen-related receptors hERRI and hERRI 
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No. 1.04e-64;
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Best Local Similarity
Matches 97; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 24; Fig I-2(1) to (2); 243pp; English.

DNAs encoding hormone receptors and the hormone receptors themselves claimed. The DNA can be used to make the hormone receptor proteins an functional modified forms in quantities not previously possible. The receptor proteins can be used to screen cpds for receptor-agonist or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant DNA encoding ho comprising glucocorticoid, rand novel hormone receptors
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23-OCT-1987; U02782.
20-OCT-1987; US-108471.
(SALK) Salk Inst for Biol Stud.
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receptor (hGR)
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Sequence 777 AA;
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Pred. No. 5.47e-46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is the amino acid sequence of a mutant nuclear glucocorticoid receptor (NGR), especially mutated in the region encoding the ligand binding domain (LBD), such that the activity of the receptor is induced more strongly by a synthetic glucocorticoid ligand than by a natural glucocorticoid ligand. The mutation is a point mutation in the coding sequence (a transition mutation) generated by site-directed mutagenesis. This causes a replacement of the Ile residue at position 747 with a Thr residue. The position lies in the region between helices 11 and 12. The mutant coding sequence is used to generate a fusion protein comprising a protein whose activity is to be regulated by and fused to the NGR sequence. The protein is preferably a recombinase, especially the Cre recombinase from bacteriophage P1 (see V05702). The sequence encoding the fusion protein, and vectors containing it, are used to treat cells either ex vivo or in vitro for use in gene therapy. Vectors containing and expressing the protein allow the transfer of heterologous genes to the cells' genome by recombinase-directed recombination at loxp sites. By using a mutated LBD, normal physiological levels of the ligand within the ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ASRE-) ASSOC DEV REC
Brocard JB, Chambon E
Nicolas JC, Roux S;
WPI; 97-451186/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mutant nuclear glucocorticoid receptor 1747T. Mutant; nuclear glucocorticoid receptor; ligal point mutation; site-directed mutagenesis; fu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W44700 standard; Protein; W44700; 12-MAY-1998 (first entry)
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ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; V05701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-FEB-1996; 002060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc_difference
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301
                                                    566
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                                                                                                                                                                                                                                                                                                                                    123
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                                                                                                                                                                                                                                                                                                                                                              lggrqviaavkwakaipgfrnlhlddqmtllqyswmflmafalgwrsyrgssanllcfap
                                                                                                                                        ylcagrndciidkirrkncpacryrkclqagmnl-earktk-k-kikgiqqattg-v-sq
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                                                                                                        GKAKRSGGHAPRVRELLLDALSPEQLVLTLLEAEPPHVLISRPSAPFTEAS---MMMSLTK
                                                                                                                                                                                                                   YICPATNQCTIDKNRRKSCQACRLRKCYEVGMVKCGSRRERCGYRLVRRQRSADEQLHCA
                                                                                                                                                                                                                                                                                                                              TLKRKVSGNRCASPVTGPGSKRDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHND
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
97; Conse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 50-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EN GENETIQUE MOLECULAIRE., Gronemeyer H, Metzger D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          777
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
Pred.
84; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glucocorticoid receptor inducible by synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    614; DB 28;
No. 5.47e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          replacement fron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ligand binding domain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 777;
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to

    and vector
glucocorticoid

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                                                                                                                                                                                                                                                                                                                                                                                        Mammalian cell having a plurality of steroid receptor response elements - can be directly detected when bound by fluorescently related steroid receptor labelied steroid receptor so claim 9; page 67-72; 100pp; English.

A fusion protein (W17789) comprises jellyfish green fluorescent protein (GFP) fused to rat glucocorticoid receptor (GR) via a Glycal repeat linker. The GFP moiety contains an S65T substn. and the GR has a C655S substn. that humanises the protein and increases contg. a number of steroid receptor response elements in array, is used to visualise directly the interaction of GR and its binding site in chromatin using the fluorescently labelled GR. This provides the direct opportunity to visualise receptor/target interactions and can be used to screen for ligands that activate
                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Green fluorescent protein gPlucocorticoid receptor fusion. Green fluorescent protein; GFP; glucocorticoid receptor; steroid receptor; transcription factor; DNA binding molecule. Chimaeric Aequoria victoria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JT 15
W17789 standard; Protein; 1070 AA.
W17789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-DEC-1996; U19516.

08-DEC-1995; US-008373.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

Hager GL, Htun H;

WPI; 97-319778/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain
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                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                nucleus of
                                                                                                                                                                                                                                                                                                                                                                             gene targetting or translocation of steroid receptors in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193
                                                                                                                                                                                                                                134
                                                                                                                                                                                                                                                              699
                                                                                      869
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 idkirrkncpacryrkclqagmn1-earktk-k-kikgiqqatag-v-sqdtsenpn-kt 812
                                                                                                                                                                                                                                  ASPVTGPGSK-RDAHFCAVCSDYASGYHYGVWSCEGCKAFFKRSIQGHNDYICPATNQCT 192
                                                                                                                                                                                                                                               -ivpaalpg-ltpt-lv-slleviepevlyagydssvpdsawrimttlnmlggrqviaav 868
                                                        SWAKKIPGFVELSLFDQVRLLESCWMEVLMMGLMWRSIDHP-GKLI-FAPDLVLDRDEGK 368
                                                                                                                 PRVRELLLDALSPEQLVLTLLEAEPPHVLISRPSAPFTEAS--MMMSLTKLADKELVHMI
                                                                                                                                                                          IDKNRRKSCQACRLRKCYEVGMVKCGSRRERCGYRLVRRQRSADEQLHCAGKAKRSGGHA 252
                                                                                                                                                                                                                                                                                        h 15.1%;
Similarity 33.2%;
93; Conservative
                                                                                                                                                                                                                                                                                                                                                  a mammalian cell.
1070 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261..270
/label= Linker
271..1070
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/note= "green fluorescent
261..270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "glucocorticoid receptor"
                                                                                                                                                                                                                                                                                        Score 590; DB 23; Length 1070; Pred. No. 1.11e-43; 83; Mismatches 88; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein"
    408
                             967
                                                                                                                                                                                                                                                                                                                   Length 1070;
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369

Search completed: Mon Job time: 199 secs. Nov N 16:27:39 1998